

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 11:39:20 ; Search time 42 seconds
(without alignments)
1356.198 Million cell updates/sec

Title: US-09-724-254A-3
Perfect score: 3124
Sequence: 1 MLNWLIVLAPVSGQFART.....AEFSLTHSKMLFALSFLP 592

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	418.5	13.4	344	A41357	Fc gamma (IGG) rec
2	418.5	13.4	374	A39878	Fc gamma (IGG) rec
3	402.5	12.9	404	A46480	Fc gamma (IGG) rec
4	396	12.7	336	I48471	Fc gamma (IGG) rec
5	326.5	10.5	296	I46021	Fc gamma (IGG) rec
6	319	10.2	270	A34636	Fc-gamma receptor
7	299.5	9.6	4391	A38096	perlecan precursor
8	292.5	9.4	254	JL0107	Fc gamma (IGG) rec
9	292	9.3	233	JU0284	Fc gamma (IGG) rec
10	290	9.3	323	S06946	Fc gamma (IGG) rec
11	289	9.3	310	JL0119	Fc gamma (IGG) rec
12	275	8.8	7962	I38346	elastic titin - hu
13	272	8.7	255	JC7593	SH2 domain-contain
14	267	8.5	257	S00682	IgE Fc receptor al
15	264.5	8.5	317	JL0118	Fc gamma (IGG) rec
16	262	8.4	285	S36903	Fc gamma (IGG) rec
17	258	8.3	3707	S18252	heparan sulfate pr
18	257	8.2	261	S29360	Fc gamma (IGG) rec
19	256	8.2	280	I55577	Fc gamma (IGG) rec
20	253.5	8.1	283	FCN5G1	Fc gamma (IGG) rec
21	253.5	8.1	330	A40071	Fc gamma (IGG) rec
22	253.5	8.1	330	I49660	Fc gamma (IGG) rec
23	252.5	8.1	1256	T03096	CDO protein - rat
24	248.5	8.0	738	A40096	platelet-endotheli
25	244	7.8	267	I56110	Fc-gamma RIIB-alp
26	241	7.7	1694	S50065	sialoadhesin - mou
27	241	7.7	1896	T08951	Down syndrome cell
28	240	7.7	1862	I49583	differentiation an
29	235.5	7.5	1240	T03097	CDO protein - huma

30 234 7.5 968 2 A46512 CD22 homolog/B lym
31 230.5 7.4 702 2 A36319 carcinoembryonic a
32 230 7.4 1026 2 I58164 BIG-1 protein - ra
33 229 7.3 267 2 A35902 Fc gamma (IGG) rec
34 229 7.3 847 2 JH0371 B-cell adhesion pr
35 229 7.3 1327 2 T09402 immunoglobulin-lik
36 227.5 7.3 1040 2 A34695 axonal glycoprotei
37 227 7.3 245 2 A30154 IgE receptor alpha
38 224.5 7.2 1323 2 PNO568 connectin 3B - chi
39 224 7.2 4162 2 T42633 connectin/titin -
40 223.5 7.2 1036 2 S22383 axonin 1 precursor
41 221.5 7.1 5175 2 T20992 hypothetical prote
42 221.5 7.1 5198 2 T43290 hemiscenin precurs
43 219 7.0 1033 2 S19247 cell adhesion prot
44 219 7.0 3375 2 T19821 hypothetical prote
45 217 6.9 1028 2 A53449 plasmacytoma-assoc

ALIGNMENTS

RESULT 1

A41357 Fc gamma (IGG) receptor I (high affinity) form b - human
N;Alternate names: CD64
C;Species: Homo sapiens (man)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A41357; S03019
R;Allen, J.M.; Seed, B
Science 243, 378-381, 1989
A;Title: Isolation and expression of functional high-affinity Fc receptor complementary
A;Reference number: A41357; MUID:89100284; PMID:2911749
A;Accession: A41357
A;Molecule type: mRNA
A;Residues: 1-344 <ALL1>
A;Cross-references: UNIPROT:P12314; GB:X14355; GB:M21090; NID:G31333; PIDN:CAA32536.1; I
R;Allen, J.M.; Seed, B, 11824, 1988
Nucleic Acids Res. 16, 11824, 1988
A;Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (Fc
A;Reference number: S03018; MUID:89098339; PMID:2974947
A;Accession: S03019
A;Molecule type: mRNA
A;Residues: 1-344 <ALL2>
A;Cross-references: ENBL:X14355; NID:G31333; PIDN:CAA32536.1; PID:G31334
A;Note: the authors translated the codon ACT for residue 25 as Ala
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
F;117-170/Domain: immunoglobulin homology <IMM>

Query Match 13.4%; Score 418.5; DB 2; Length 344;
Best Local Similarity 37.0%; Pred. No. 8.2e-21;
Matches 108; Conservative 41; Mismatches 122; Indels 21; Gaps 10;

QY 1 MLNWLIVLAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGRFYSPOKTKWYHR 60
Db 7 LLLMW-----FVDDQ-VDTTKAVITIQPPWVSFQEETVTLRCEVHLHPGSSSTQFLN 59
QY 61 YLGRKILRETPD---NILEVQESGEYRCQAGSFLSPVHLDFSSASLILQAPLSVF-EG 116
Db 60 --GTATQTSTPSYRITTSASVNDSGEYRCQGLSGRSDPIQLIEHTRGWLILQVSSRVFTEG 117
QY 117 DSVVLRCRA-KAEVTLNNTIYKNDNLVLAFLNKRDTDFHHPACLKDNCAVRCCTGYKSSCCP 175
Db 118 SPLAURCHAWKDKLVYVNLVYRNGKAFKFFHWSNLTKTNISHNGTHVCSGNGKH--R 175
QY 176 VSSNTVKIQVQEPFTRPVLIRASSFQP-ISGNPVTLTCTETQLSLERSDVLPRPFRDDQT 234
Db 176 YTSAGISVTYKELFPAPVLNASVTSPLLEGNLVLTSCETKLLQRPGLQLYFYSFGMSKT 235
QY 235 LGLGWSLSPNQITAMWSKDSGFYWCXKAATMPHSVIDSPRSWTQV---QIP 283
Db 236 L-RGNTSSEIQILTRARSDSLYFCAATEDGNVLKRSFELQVLGLQLP 286

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RESULT 2
A38878
Fc gamma (IgG) receptor I-A (high affinity) precursor - human
N:Alternate names: CD64
C:Species: Homo sapiens (man)
C>Date: 30-Dec-1991 #sequence revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: A39878; 170304; E41357; S03018; I57525
R:van de Winkel, J.G.J.; Ernst, L.K.; Anderson, C.L.; Chiu, I.M.
J. Biol. Chem. 266, 13449-13455, 1991
A:Title: Gene organization of the human high affinity receptor for IgG, Fc gamma RI (CD64)
A:Reference number: A39878; MUID:91320383; PMID:1830050
A:Accession: A39878
A:Molecule type: DNA
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:Q92663; GB:M63830; GB:M63835; NID:G180277; PIDN:AAA35678.1;
R:Forges, A.J.; Redecha, P.B.; Doebele, R.; Fan, L.C.; Salmon, J.E.; Kimberly, R.P.
J. Clin. Invest. 90, 2102-2109, 1992
A:Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.
A:Reference number: I55577; MUID:93055454; PMID:1430234
A:Accession: I70304
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: GB:L03418; NID:G184840; PIDN:AAA36049.1; PID:G292169
R:Allen, J.M.; Seed, B.
Science 243, 378-381, 1989
A:Title: Isolation and expression of functional high-affinity Fc receptor complementary
A:Reference number: A41357; MUID:89100284; PMID:2911749
A:Accession: B41357
A:Molecule type: mRNA
A:Residues: 1-24, 'S', '26-337', 'T', '339-374' <AL1>
A:Cross-references: GB:X14356; GB:M21091; NID:G31331; PIDN:CAA32537.1; PID:G31332
R:Allen, J.M.; Seed, B.
Nucleic Acids Res. 16, 11824, 1988
A:Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FcR)
A:Reference number: S03018; MUID:89098339; PMID:2974947
A:Accession: S03018
A:Molecule type: mRNA
A:Residues: 1-24, 'S', '26-337', 'T', '339-374' <AL2>
A:Cross-references: EMBL:X14356; NID:G31331; PIDN:CAA32537.1; PID:G31332
R:Perez, C.; Wietzerbin, J.; Benech, P.D.
Mol. Cell. Biol. 13, 2182-2192, 1993
A:Title: Two cis-DNA elements involved in myeloid-cell-specific expression and gamma int
ism.
A:Reference number: I57525; MUID:93204964; PMID:8455606
A:Accession: I57525
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <RE2>
A:Cross-references: GB:S57204; NID:G2986692; PIDN:AAD13887.1; PID:G4261587
C:Genetics:
A:Gene: GDB:FCGR1A; CD64
A:Cross-references: GDB:135911; OMIM:146760
A:Map position: 1q21-1q21
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane P
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-292/Domain: extracellular #status predicted <EXT>
F;117-170/Domain: immunoglobulin homology <IMM2>
F;293-313/Domain: transmembrane #status predicted <TM>
F;59,78,152,159,163,195,240/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 13.4%; Score 418.5; DB 1; Length 374;
Best Local Similarity 37.0%; Pred. No. 9.1e-21;
Matches 106; Conservative 41; Mismatches 122; Indels 21; Gaps 10;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPWTVTFQGERVTLTKCKGFRFYSQKTKWYHR 60
|||||
DB 7 LLLWV-----PVDGQ-VDTTKAVITLQPPWVSVFQEEIVTLHCEVHLPLGSSSTQWFLN 59
|||||
QY 61 YLGEILRETPD---NILEVQESGEYRCQAQSPSSPVHLDFSSASLILQAPLSVP-EG 116
|||||

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DB 60 --GTATQTPTSPYRITSASVNDSGEYRCQGLSGRSDPIQLIHRGWLLOVSSRVFTG 117
QY 117 DSVVLRCRA-KABVTLNNTIYKNDVLAFLNKRTPHIFACLKONGKAYRCYKESCCP 175
|||
DB 118 EPLALRCHAWKOKLVYVLYENGKAFKFFHNSNLITLKTNIHNGYHCSGMKH--R 175
|||
QY 176 VSSNTVKIQVQEPTRPVLRASFPQ-ISGNPVTLTCETQLSLERSDVLPRFRFRDQ 234
|||
DB 176 YTSAGISVTVKELFFAPVLRASVTPSLLEGNLVLTSCETKLLQRPGLQLYSFYMGSKT 235
|||
QY 235 LGLGWSLSPNFOTAMWSKDSGFYCKAATMPSHVISDSPRWIOV---QIP 283
|||
DB 236 L-RGRNTSSEYQLITARRRDSGLYWCERATDGNVKRSPELEQLVGLQLP 286
|||
RESULT 3
Fc gamma (IgG) receptor high affinity - mouse
N:Alternate names: high affinity IgG receptor
C:Species: Mus musculus (house mouse)
C>Date: 18-Jun-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46480; A43511
R:Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.
J. Immunol. 148, 1570-1575, 1992
A:Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and
A:Reference number: A46480; MUID:92166399; PMID:1531670
A:Accession: A46480
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-404 <OSM>
A:Cross-references: UNIPROT:P26151
A:Note: sequence extracted from NCB1 backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NC
R:Sears, D.W.; Osman, N.; Tace, B.; McKenzie, I.F.C.; Hogarth, P.M.
J. Immunol. 144, 371-378, 1990
A:Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG
A:Reference number: A43511; MUID:90111035; PMID:2136886
A:Accession: A43511
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <SEA>
A:Cross-references: GB:M31314; NID:G200752; PIDN:AAA40056.1; PID:G200753
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F;127-179/Domain: immunoglobulin homology <IMM>
Query Match 12.9%; Score 402.5; DB 2; Length 404;
Best Local Similarity 36.3%; Pred. No. 1.2e-19;
Matches 107; Conservative 42; Mismatches 131; Indels 15; Gaps 10;
QY 3 LWVI--LLVLPVSGQFARTPRPIIFLQPPWTVTFQGERVTLTKCKGFRFYSQKTKWYHR 60
|||
DB 10 MWLLTLLLVVPGVGVNATKAVITLQPPWVSIFQENVTLCWCEGPHLPDGSSTQWFIN 69
|||
QY 61 YLGEILRETPDNL---EVQESGEYRCQAQSPSSPVHLDFSSASLILQAPLSVP-EG 116
|||
DB 70 --GTAVQISTFSYIPEASFDQSGEYRCQIGSSMPSDPVQLQHNDWLLQLQASRRVLTEG 127
|||
QY 117 DSVVLRCRA-KAEVTLNNTIYKNDVLAFLNKRTPHIFACLKONGKAYRCYKESCCP 175
|||
DB 128 EPLALRCHGWKLVYVLYENGKAFKFFHNSNLITLKTNIHNGYHCSGMKH--R 184
|||
QY 176 VSSNTVKIQVQEPTRPVLRASFPQI-SGNPVTLTCETQLSLERSDVLPRFRFRDQ 234
|||
DB 185 YTSAGISVTVKELFTPLVLRASVSSPPPEGSLVTLNCETNLLQRPGLQLYSFYMGSKI 244
|||
QY 235 LGLGWSLSPNFQITAMWSKDSGFYCKAATMPSHVISDSPRWIOVQIP-ASHPV 288
|||
DB 245 LEYR-NTSSSYHTARAREDAAGFYWCVEATDSSVLKRSFELEQLVGLPOSSAPV 298
|||
RESULT 4
148471
Fc gamma (IgG) receptor high affinity - mouse

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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I48471
R;Prins, J.B.; Todd, J.A.; Rodrigues, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Gaff
Science 260, 695-698, 1993
A;Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Ig
A;Reference number: I48471; MUID:93242399; PMID:8480181
A;Accession: I48471
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-336 <RES>
A;Cross-references: EMBL:X70980; NID:G311748; PIDN:CAA50311.1; PID:G311749
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: immunoglobulin receptor
F;128-180/Domain: immunoglobulin homology <IMM>

Query Match 12.7%; Score 396; DB 2; Length 336;
Best Local Similarity 36.1%; Pred. No. 2.6e-19;
Matches 108; Conservative 43; Mismatches 130; Indels 18; Gaps 12;
Qy 3 LWI--LLVLAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSQKTKVHR 60
Db 10 MLLTLLLLVPPVGGVWNAKAVITLQPPWASIFQKENVTLWCSEPHLPGDSSTQWFN 69
Qy 61 YLKEILRETPD---NILEQSEGYRCQAQSPSSPVHLDFFSSA-LILQAPLSVP-E 115
Db 70 --GTWQTSPTSYSISVASFQDSGEYRCQIGSSVPSDPVQLQIHKEDWLLQASRRVLTE 127
Qy 116 GDSVILRCRA-KAEVILNTIYKQDNVLAFLNKRTPDHPHACLKDNQAYRCTG---YKE 171
Db 128 GEPLAURCHGKRNKLVYVNVFRNGSKFKP-SGSKIALKLNLSHSGIYHCSGNRHY 186
Qy 172 SCCPVSSNTVKIQVQFPTRPVLRASSFOPI-SGNPVTLTCTQSLERSDVPLFRFRFR 230
Db 187 TSAGVSI-TVKAPFLELFTPLVLRASVSPPFEGSLVTLNCTELLQRLPGQLYFSYV 245
Qy 231 DDQTLGLGWSLNFQITAMWSDGFYCKATMPHSVISDPSRWTVQVQIP-ASHPV 288
Db 246 GSKILEYR-NTSEYHIAEREDAGFYCEVATEDSSVLKHSPLKLEQLVQSSAPV 303

RESULT 5
I46021
Fc-gamma receptor II - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I46021; S40204
R;Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.
Immunogenetics 39, 423-427, 1994
A;Title: Cattle Fc gamma RII: molecular cloning and ligand specificity.
A;Reference number: I46021; MUID:94245284; PMID:8188320
A;Accession: I46021
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-296 <ZHA>
A;Cross-references: UNIPROT:Q28110; EMBL:X75671; NID:G437978; PIDN:CAA53367.1; PID:G4379
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor

Query Match 10.5%; Score 326.5; DB 2; Length 296;
Best Local Similarity 37.0%; Pred. No. 1e-14;
Matches 90; Conservative 34; Mismatches 100; Indels 19; Gaps 10;
Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSQKTKVHR 60
Db 28 MLLWTALLFLAPVSGK-PDLPRAVVTIQAWINVLREDHVTILTCGTGTSFAGNLTWPHN 86
Qy 61 YLKEILRETPDNIIEV--QSEGYRCQAQSPSSPVHLDFFSSASILLQAPLSVP-EG 116
Db 87 --GSSHTQKQPSYFRAGNSGYSRCQREQTSLSDPVHLDVLSDWLLQTLPSLVQEG 144
Qy 117 DSVVLRCRAKAEVTLNN--TIYKNDNVLAFLNKRTPDHPHACLKDNQAYRCTGYESCCP 175

Db 145 EPIMLRCHSWRNQPLNKITFYQDRKSKIFSQVORTNFSIPRANLHSGQYHCTAFIGKMLH 204
Qy 176 VGSNTVKIQVQFPTRPVLRASSFOPIGNPVTLTCTQSLERSDVPLFRFRFRDDQT 234
Db 205 --SQPNVITVQE-----SSSGPSSWTAIVAGTCFAAVALVAIITW-FRLRRPIS 254
Qy 235 LGL 237
Db 255 AGL 257
RESULT 6
A34636
Fc-gamma receptor II precursor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
C;Accession: A34636
R;Tomimaga, M.; Sakata, A.; Ohmura, T.; Yamashita, T.; Koyama, J.; Onoue, K.
Biochem. Biophys. Res. Commun. 168, 683-689, 1990
A;Title: The structure and expression of the guinea pig Fc receptor for IgG1 and IgG2 (I
A;Reference number: A34636; MUID:90241239; PMID:1692213
A;Accession: A34636
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-270 <TOM>
A;Cross-references: GB:M35272
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor
F;37-88/Domain: immunoglobulin homology <IMM>

Query Match 10.2%; Score 31.9; DB 2; Length 270;
Best Local Similarity 35.6%; Pred. No. 2.9e-14;
Matches 84; Conservative 28; Mismatches 72; Indels 52; Gaps 8;
Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSQKTKVHR 60
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSQKTKVHR 60
Qy 61 YLKEILRETPDNIIEV--QSEGYRCQAQSPSSPVHLDFFSSASILLQAPLSV 113
Db 61 --GRLI---PTQVLFSYRFTAKGNDGSEYRCAGGTSLSDPVRLDVLSDWLVLTQSLI 114
Qy 114 F-EGDSVILRCRAKAEVTLNN-----TIYKNDNVLAFLNKRTPDHPHACLKDNQAYRC 166
Db 115 FEGDVILURCH-----SWNNWPLAKVTIFYHNGVAKYFYSIKNFSIDQAHSHSGAYNC 169
Qy 167 TGYKESCCPVSSNTVKIQVQFPTRPVLRASSFOPIGNPVTLTCTQSLERSDV 222
Db 170 TGL-----IGRTSHTSP-----PVTITVQGPKSSDSMW 198

RESULT 7
A38096
perlecan precursor - human
N;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prot
C;Species: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 12-Jul-2004
C;Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736
R;Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
J. Biol. Chem. 267, 8544-8557, 1992
A;Title: Primary structure of the human heparan sulfate proteoglycan from basement memb
tor, laminin, neural cell adhesion molecules, and epidermal growth factor.
A;Reference number: A38096; MUID:92235084; PMID:1569102
A;Accession: A38096
A;Molecule type: mRNA
A;Residues: 1-4391 <MUR>
A;Cross-references: UNIPROT:P98160; GB:M85289; NID:G184426; PIDN:AAA52700.1; PID:G18442
R;Kallunki, P.; Tryggvason, K.
J. Cell Biol. 116, 559-571, 1992
A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD pr
cell adhesion molecules, and epidermal growth factor.
A;Reference number: A41736; MUID:92112994; PMID:1730768
A;Accession: S19256

A:Molecule type: mRNA
 A:Residues: 1-57, 'D', 59-434, 'A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R', 71-2979, 'H', 2981-2994, 'G', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-3711, 'R', 3713-3714, 'R', 3716-3717, 'R', 3719-3720, 'R', 3722-3723, 'R', 3725-3726, 'R', 3729-3730, 'R', 3733-3734, 'R', 3737-3738, 'R', 3741-3742, 'R', 3745-3746, 'R', 3749-3750, 'R', 3753-3754, 'R', 3757-3758, 'R', 3761-3762, 'R', 3765-3766, 'R', 3769-3770, 'R', 3773-3774, 'R', 3777-3778, 'R', 3781-3782, 'R', 3785-3786, 'R', 3789-3790, 'R', 3793-3794, 'R', 3797-3798, 'R', 3801-3802, 'R', 3805-3806, 'R', 3809-3810, 'R', 3813-3814, 'R', 3817-3818, 'R', 3821-3822, 'R', 3825-3826, 'R', 3829-3830, 'R', 3833-3834, 'R', 3837-3838, 'R', 3841-3842, 'R', 3845-3846, 'R', 3849-3850, 'R', 3853-3854, 'R', 3857-3858, 'R', 3861-3862, 'R', 3865-3866, 'R', 3869-3870, 'R', 3873-3874, 'R', 3877-3878, 'R', 3881-3882, 'R', 3885-3886, 'R', 3889-3890, 'R', 3893-3894, 'R', 3897-3898, 'R', 3901-3902, 'R', 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RESULT 10

S06946
Fc gamma (IgG) receptor - human
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: S06946
R:Stuart, S.G.; Simister, N.E.; Clarkson, S.B.; Kacinski, B.M.; Shapiro, M.; Wellman, I.
EMBO J. 8, 3657-3666, 1989
A:Title: Human IgG Fc receptor (hFCRII; CD32) exists as multiple isoforms in macrophages
A:Reference number: S06946; MUID:90059965; PMID:2531080
A:Accession: S06946
A:Molecule type: mRNA
A:Residues: 1-323 <STU>
A:Cross-references: UNIPROT:P31995; EMBL:X17652; NID:G32073; PIDN:CAA35642.1; PID:G32074
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F:64-115/Domain: immunoglobulin homology <IMM>

Query Match 9.3%; Score 290; DB 2; Length 323;
Best Local Similarity 36.3%; Pred. No. 3.2e-12;
Matches 74; Conservative 26; Mismatches 84; Indels 20; Gaps 6;
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
DB 28 MLLWTAVLFLAPVAGTAPPAAPKAVLKLEPQWVNLQEDSVLTLCRGTHSPESDSIQWFHN 87
QY 61 YLGKEILRETDPNI---LEVOSEGEYRCQAGSPLSPVHLDFSSASLILOAP-LSVFEG 116
DB 88 --GNLIPHTOPSVRFRKANNDSGEYTCQTGTSLSDPVHLTVLSEWLVLTQPHLEFQEG 145
QY 117 DSVVLRCRA-KAEVTLNNTIYKNDVLAFLNKRDTDFHIFACLDKNGAYRCTG-----Y 169
DB 146 ETIVLRCHSWDKPLVKVTFPQNGSKKFSRSDNFSIPQANHSHSGDYHCTGNIGVTLY 205
QY 170 KESCCPVSSNTVKIQVQEPFTRPV 193
DB 206 -----SSKPVTTIVQAPSSPM 222

RESULT 11

JL0119
Fc gamma (IgG) receptor IIB precursor - human
X:Alternate names: Fc gamma (IgG) receptor II (low affinity) beta; surface glycoprotein
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JL0119; A43543; A60568; A45877; S00478
R:Brooks, D.G.; Qiu, W.Q.; Luster, A.D.; Ravetch, J.V.
J. Exp. Med. 170, 1369-1385, 1989
A:Title: Structure and expression of human IgG FcRII (CD32): functional heterogeneity is
A:Reference number: JL0118; MUID:90010791; PMID:2529342
A:Accession: JL0119
A:Molecule type: mRNA
A:Residues: 1-310 <BRO>
A:Cross-references: UNIPROT:P31994
R:Engelhardt, W.; Geerts, C.; Frey, J.
Eur. J. Immunol. 20, 1367-1377, 1990
A:Title: Distribution, inducibility and biological function of the cloned and expressed
A:Reference number: A43543; MUID:90316181; PMID:2142460
A:Accession: A43543
A:Molecule type: mRNA
A:Residues: 1-204, 'Y', 206-254, 274-310 <ENG>
A:Cross-references: GB:X52473; NID:G328171; PIDN:CAA36713.1; PID:G29428
R:Engelhardt, W.; Geerts, C.; Frey, J.
Mol. Immunol. 27, 379-387, 1990
A:Title: Organization of human FCRII and FCRII-like (betaFCRII) genes: structural homolo
A:Reference number: A60568; MUID:90294837; PMID:2141667
A:Accession: A60568
A:Molecule type: DNA
A:Residues: 1-38 <EN2>
R:Seki, T.
Immunogenetics 30, 5-12, 1989
A:Title: Identification of multiple isoforms of the low-affinity human IgG Fc receptor.
A:Reference number: A45877; MUID:89307398; PMID:2526077

A:Accession: A45877
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-74, 'Q', '76-119, 'V', 121-204, 'Y', 206-231, 'T', 233-254, 274-310 <SBK>
A:Cross-references: GB:M88696; NID:G184843; PIDN:AAA36051.1; PID:G306929
A>Note: the authors translated the codon CAG for residue 75 has His
R:Stangelin, S.; Stamenkovic, I.; Seed, B.
EMBO J. 7, 1053-1059, 1988
A:Title: Isolation of cDNAs for two distinct human Fc receptors by ligand affinity cloning
A:Reference number: S00477; MUID:88296409; PMID:3402431
A:Accession: S00478
A>Status: not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 1-35, 'S', 37-204, 'Y', 206-253, 'G', 255 <STB>
A>Note: the authors suggest that the cDNA is derived from a precursor RNA that still con
C:Genetics:
A:Gene: GDB:FCGR2B; FCGR2; FCGR2
A:Cross-references: GDB:I28183; OMIM:146790
A:Map position: 1Q23-1Q23
A:Introns: 131/1
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: alternative splicing; glycoprotein; immunoglobulin; immunoglobulin receptor;
F:1-44/Domain: signal sequence #status predicted <SIG>
F:45-310/Product: IgG Fc receptor IIB #status predicted <MAT>
F:45-222/Domain: extracellular #status predicted <EXT>
F:64-115/Domain: immunoglobulin homology <IMM1>
F:145-198/Domain: immunoglobulin homology <IMM2>
F:223-245/Domain: transmembrane #status predicted <TM>
F:246-310/Domain: intracellular #status predicted <INT>
F:106,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.3%; Score 289; DB 2; Length 310;
Best Local Similarity 36.9%; Pred. No. 3.6e-12;
Matches 73; Conservative 26; Mismatches 91; Indels 8; Gaps 5;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
DB 28 MLLWTAVLFLAPVAGTAPPAAPKAVLKLEPQWVNLQEDSVLTLCRGTHSPESDSIQWFHN 87
QY 61 YLGKEILRETDPNI---LEVOSEGEYRCQAGSPLSPVHLDFSSASLILOAP-LSVFEG 116
DB 88 --GNLIPHTOPSVRFRKANNDSGEYTCQTGTSLSDPVHLTVLSEWLVLTQPHLEFQEG 145
QY 117 DSVVLRCRA-KAEVTLNNTIYKNDVLAFLNKRDTDFHIFACLDKNGAYRCTGKESCCP 175
DB 146 ETIVLRCHSWDKPLVKVTFPQNGSKKFSRSDNFSIPQANHSHSGDYHCTG-NIGYTL 204
QY 176 VSSNTVKIQVQEPFTRPV 193
DB 205 FSSKPVTTIVQAPSSPM 222

RESULT 12

I38346
elastic titin - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I38346
R:Rabeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A:Reference number: A57430; MUID:96026330; PMID:7569978
A:Accession: I38346
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-7962 <RES>
A:Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:G1017426; PIDN:CAA62189.1; PID:G101
C:Genetics:
A:Gene: GDB:TTN
A:Cross-references: GDB:I27867; OMIM:188840
A:Map position: 2q31-2q31
Query Match 8.8%; Score 275; DB 2; Length 7962;

Best Local Similarity 25.0%; Pred. No. 2e-09;
Matches 150; Conservative 71; Mismatches 262; Indels 116; Gaps 27;

QY 23 PIFLOPPPTTPOGRRVTLTC-----KGRFYSPOKTKYHYRLOKEILRE 69
DB 216 PTFSLRPKSLTTFVGKAARPICTVGTPTVETIWKDGAALSPSPNWRISDAENKHILEL 275
QY 70 TPDNILEVQESGYRCQAQGSPLSPVHLDFSSASLIL-----QAPLSVFEGDSVV 120
DB 276 SN---LTIQDRGVYSCKA-----SNKFGADICQAEILLIDKPHFIKELEPQSAINKKVH 327
QY 121 LRCA-----KAETVLTNTIYK-----NDNVLAFLNKRTHFPHACLKONGAYRCTGYKES 172
DB 328 LECQVDEDRKVTWTGSKQCKLPQKDYKICFEDXIATLEPLAKLKDSGYTVCAGNEA 387
QY 173 CCPVSSNTVKIQVCEFTFPVLRASSFQISGNPVTLCETQLSLERSDVPLRRFRFRDD 232
DB 388 GSSCCCATVTVREPPSFVKV---DPSYLMPLGESARLHCK---LKGSPV-IQVTPKNN 440
QY 233 QTLGLGWSLSPN-----QTAMWSKDSGYKCAATMPHSVILSDSPRSWIOVQIPAS 285
DB 441 KELSENTVRMYFVNSEAILDITDKVEDSGSYSCAV---NDVGSDDSCSTEIVIKPPPS 497
QY 286 HPVLTLSPEKALNFEQTKVTLHCET-----QEDSLRT---LYRFVHEGVPLRHK 331
DB 498 F-IKLEPADIV---RGTNALLQCEVSGTCGPFISWFKKQIRSSKVRLESQ-----K 548
QY 332 SVRCERGAISPLTTEGNSGYCTADNGLGAKPKSVLSVTVPVSHVNLNLSDBDLI 391
DB 549 SLVCLSE---LFSNSADYGEYCVVANEVGGCGMATHL-----LKBPPTFVKKVDLI 599
QY 392 FEGAKVTLHCEAQRGSLPIL-----YQPHHEDAALERSANSAGVNAISF---SLTAHS 443
DB 600 ALGGQIVTLQAAVGESEPSVMTWKQGVIREGKIKSPFN---GVAVLIPDVQISFG 656
QY 444 GNYCTADNGFGPQRSKAVLSITVPVSHVTLTSSAAL-TFEGATVTLHCRVQORSPQ 502
DB 657 GRYTCLAENAGSQTSGELI-----VKPAKIIERAEILQVTDGPAITLEYTV-AGTPE 710
QY 503 ILVCFVHEMDPLVSSSTPSVGRVSF-----SFLSTEGH-SGNVYCTADNGFGPQRSSE 553
DB 711 LKPKWYKDRPLVASKK---YRISFNNVAQLKFSYSELHDSGGQVTFISNEVGSSCE 766

RESULT 13
JC7593
SH2 domain-containing phosphatase anchor protein 1a - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7593
A:Title: Molecular cloning and characterization of SPAP1, an inhibitory receptor.
A:Reference number: JC7593; MUID:21092675; PMID:11162587
A:Accession: JC7593
A:Molecule type: mRNA
A:Residues: 1-255 <XUA>
A:Cross-references: UNIPROT:Q9BZ16; GB:AF319438
C:Genetics:
A:Gene: spapia
A:Map position: 1q21
A:Introns: 135/1; 174/1; 183/2; 212/1; 234/1; 243/3
C:Keywords: glycoprotein
F:27-135/Domain: extracellular #status predicted <EXT>
F:68-115/Domain: immunoglobulin-like #status predicted <IGL>
F:148-169/Domain: transmembrane region #status predicted <TM>
F:195-255/Domain: intracellular #status predicted <INT>

Query Match 8.7%; Score 272; DB 2; Length 255;
Best Local Similarity 57.6%; Pred. No. 3.8e-11;
Matches 57; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

QY 371 LSVTVPSVHVLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDDALERSANSAG 430

DB 38 LCLSVVSPVTLSPQAQAAVGDLLHCEALRGSPPILYQFYHEDVTLGNSASGSG 97
QY 431 GVAISFSLTAHSGNYCTADNGFGPQRSKAVLSITVP 469
DB 98 GASFNLSLTAHSGNYSCAANGLGAQCEAVPVVISGP 136

RESULT 14
S00682
IGF Fc receptor alpha chain precursor - human
N:Alternate names: Fc-epsilon receptor
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: S00682; B30154; S42209
R:Kochan, J.; Pattine, L.F.; Hakimi, J.; Kishi, K.; Kinet, J.P.
Nucleic Acids Res. 16; 3584; 1988
A:Title: Isolation of the gene coding for the alpha subunit of the human high affinity
A:Reference number: S00682; MUID:86233953; PMID:2967464
A:Accession: S00682
A:Molecule type: mRNA
A:Residues: 1-257 <KOC>
A:Cross-references: UNIPROT:P12319; EMBL:X06948; NID:G31317; PIDN:CAA30025.1; PID:G3131
R:Shinizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.
Proc. Natl. Acad. Sci. U.S.A. 85; 1907-1911; 1988
A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characteriza
A:Reference number: A94191; MUID:88158102; PMID:2964640
A:Accession: B30154
A:Molecule type: mRNA
A:Residues: 1-257 <SHI>
A:Cross-references: GB:J03605; NID:G187449; PIDN:AAA36204.1; PID:G307164
R:Yagi, S.; Yanagida, M.; Tanida, I.; Hasegawa, A.; Okumura, K.; Ra, C.
Eur. J. Biochem. 220; 593-598; 1994
A:Title: High-level expression of the truncated alpha chain of human high-affinity recei
nant product.
A:Reference number: S42209; MUID:94170811; PMID:8125119
A:Accession: S42209
A:Molecule type: protein
A:Residues: 26-197 <YAG>
A:Experimental source: purified recombinant protein
C:Genetics:
A:Gene: GDF:FCER1A
A:Cross-references: GDB:119902; OMIM:147140
A:Map position: 1q23-1q23
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-257/Product: IGF Fc receptor alpha chain #status predicted <MAT>
F:44-95/Domain: immunoglobulin homology <IMM1>
F:125-178/Domain: immunoglobulin homology <IMM2>

Query Match 8.5%; Score 267; DB 2; Length 257;
Best Local Similarity 37.0%; Pred. No. 8.4e-11;
Matches 64; Conservative 26; Mismatches 73; Indels 10; Gaps 5;

QY 2 LILWILLVLAVSGOFATPPIIFLOPPWTFVQGGRTVTCGFFYFQPKTKWHRY 61
DB 10 LLCVALLFFAP-DGVLAVPQPKVSLAPPWNRIFKGNVTLTCNGNFFVSVSTKWHF-- 66
QY 62 LGKEILRETPDNI-----LEVQESGYRCQAQGSPLSPVHLDFSSASLILQAPLS-VFEG 116
DB 67 -NGSLSEETSSNLINAKFEDSGEYKCOHQVNESEPVYLEVFDWLLQLQASAEVVMG 125
QY 117 DSVILRCRAKAEVTLNNTI-YKNDNVLAFLNKRTHFPHACLKONGAYRCTG 168
DB 126 QPLFLRCHGRNWDVYKVIYKDGKALKYWYENHISITNATVEDSGTYCTG 178

RESULT 15
JL0118
Fc gamma (IG) receptor Iia precursor - human
N:Alternate names: Fc gamma (IG) receptor II (low affinity) alpha; surface glycoprotein
C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 09-Jul-2004
 A:Accession: J01018; A1932; S02297; B45877; S00477; S02296
 R:Brooks, D.G.; Qiu, W.Q.; Luster, A.D.; Ravetch, J.V.
 J. Exp. Med. 170, 1369-1385, 1989
 A>Title: Structure and expression of human IgG FcR2 (CD32): functional heterogeneity is
 A:Reference number: J01018; MUID:90010791; PMID:2529342
 A:Accession: J01018
 A:Molecule type: mRNA
 A:Residues: 1-317 <BRO>
 A:Cross-references: UNIPROT:P12318; GB:M31932; NID:G182473; PIDN:AAA35827.1; PID:G182474
 A:Experimental source: placenta
 A>Note: it is uncertain whether Met-1, Met-3, or Met-7 is the initiator
 R:Hibbs, M.B.; Bonadonna, L.; Scott, B.M.; McKenzie, I.F.C.; Hogarth, P.M.
 Proc. Natl. Acad. Sci. U.S.A. 85, 2240-2244, 1988
 A>Title: Molecular cloning of a human immunoglobulin G Fc receptor.
 A:Reference number: S02296; MUID:88176920; PMID:2955389
 A:Accession: A31932
 A:Molecule type: mRNA
 A:Residues: 3-317 <HIB>
 A:Cross-references: EMBL:J03619; NID:G183619; PIDN:AAA35932.1; PID:G306803
 R:Stuart, S.G.; Trounstein, M.L.; Vaux, D.J.T.; Koch, T.; Martens, C.L.; Mellman, I.; Mc
 J. Exp. Med. 166, 1668-1684, 1987
 A>Title: Isolation and expression of cDNA clones encoding a human receptor for IgG (Fc-
 A:Reference number: S02297; MUID:88061079; PMID:2824655
 A:Accession: S02297
 A:Molecule type: mRNA
 A:Residues: 1, 7, 3-317 <STU>
 A:Cross-references: EMBL:Y00644; NID:G31335; PIDN:CAA68672.1; PID:G31336
 A>Note: it is uncertain whether Met-1 or Met-7 is the initiator
 R:Seki, T.
 Immunogenetics 30, 5-12, 1989
 A>Title: Identification of multiple isoforms of the low-affinity human IgG Fc receptor.
 A:Reference number: A45877; MUID:89307398; PMID:2526077
 A:Accession: B45877
 A:Molecule type: mRNA
 A:Status: Preliminary
 A:Residues: 7-317 <SEK>
 A:Cross-references: GB:M28697; NID:G184841; PIDN:AAA36050.1; PID:G306928
 R:Stangelin, S.; Stamenkovic, I.; Seed, B.
 EMBO J. 7, 1053-1059, 1988
 A>Title: Isolation of cDNAs for two distinct human Fc receptors by ligand affinity clon
 A:Reference number: S00477; MUID:88296409; PMID:3402431
 A:Contents: clone PC23
 A:Accession: S00477
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 7-317 <STE>
 C:Genetics:
 A:Gene: GDB:FCGR2A
 A:Cross-references: GDB:I19903; OMIM:146790
 A:Map position: 1q23-1q23
 C:Superfamily: FC gamma receptor III; immunoglobulin homology
 C:Keywords: glycoprotein; immunoglobulin receptor; transmembrane protein
 F:1-35/Domain: signal sequence #status predicted <SIG>
 F:36-317/Product: IgG Fc receptor Iia #status predicted <REI>
 F:36-216/Domain: extracellular #status predicted <EXT>
 F:55-106/Domain: immunoglobulin homology <IMW1>
 F:136-189/Domain: immunoglobulin homology <IMW2>
 F:217-240/Domain: transmembrane #status predicted <TMW>
 F:241-317/Domain: intracellular #status predicted <INT>
 F:97,178/Binding site: carbohydrate (Asn) #status predicted

Query Match 8.5%; Score 264.5; DB 2; Length 317;
 Best Local Similarity 35.7%; Pred. No. 1.6e-10;
 Matches 70; Conservative 25; Mismatches 88; Indels 13; Gaps 6;

Qy 3 LWV-----ILLVLAPVSGQAPRPIFLQPPWTFVQGERVTLTKGRFYSPQKTKW 57
 Db 16 LWLQPLTVLLLASADSQAAPKAVLEPPWVNLQEDSVTLTCQARFESDSIQW 75
 Qy 58 YHYLKGKILRETPDNI---LEVQESGEYRCQAGSPLSPVHLDFSSASLIQAP-LSW 113
 Db 76 FHN--GNLITHTQPSYRFKANNNDSEYTCQTGTSLSLDPVHLTVLSEWLVLTQPHLEF 133

QY 114 PEGDSVWLRCRA-KAEVTLNNTIYKNDNLVLAFLNKRITDFHIPHACLKNDGAYRCTGYKES 172
 DB 134 QEGETIMLRCHSWKDKPLVKVYTFQNGKSKQKFSRLDPTFSIPQANHSHSGDYHCTG-NIG 192
 QY 173 CCFVSSNTVVKIQVQEP 188
 DB 193 YTLFSSKPVITTVQVP 208

Search completed: November 30, 2004, 11:51:09
 Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 11:28:00 ; Search time 198 Seconds
(without alignments)
1720.312 Million cell updates/sec

Title: US-09-724-254A-3

Perfect score: 3124

Sequence: 1 MLLWVLLVLPVSGQFART.....AEFSLTHSKNLPALSSFLP 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2949	94.4	977	2 Q96RD9	Q96rd9 homo sapien
2	1193.5	38.2	734	2 Q96LA4	Q96la4 homo sapien
3	1193.5	38.2	734	2 Q96P31	Q96p31 homo sapien
4	1193.5	38.2	742	2 Q96S2	Q96s2 homo sapien
5	1186.5	38.0	740	2 Q96P29	Q96p29 homo sapien
6	927.5	29.7	582	2 Q80WN2	Q80wn2 mus musculu
7	847.5	27.1	639	2 Q96P30	Q96p30 homo sapien
8	826.5	26.5	515	2 Q96P35	Q96p35 homo sapien
9	820.5	26.3	515	2 Q96RE0	Q96re0 homo sapien
10	773.5	24.8	508	2 Q96LA5	Q96la5 homo sapien
11	773.5	24.8	508	2 AAQ88497	AAQ88497 homo sapi
12	772	24.7	360	2 Q8N732	Q8n732 homo sapien
13	692.5	22.2	508	2 Q8EUA5	Q8eua5 mus musculu
14	657.5	21.0	437	2 Q8NF56	Q8nf56 homo sapien
15	600.5	19.2	509	2 Q96QY5	Q96qy5 m mman-g pr
16	599.5	19.2	509	2 Q91YK7	Q91yk7 mus musculu
17	565	18.1	428	2 Q96P36	Q96p36 homo sapien
18	565	18.1	429	2 Q96LA6	Q96la6 homo sapien
19	548	17.5	124	2 Q8U746	Q8u746 homo sapien
20	548	17.5	124	2 AAQ88452	AAQ88452 homo sapi
21	548	17.5	366	2 Q8N759	Q8n759 homo sapien
22	543.5	17.4	154	2 Q8N733	Q8n733 homo sapien
23	537.5	17.2	422	2 Q96P33	Q96p33 homo sapien
24	452	14.5	722	2 Q6CNB3	Q6cnb3 xenopus lae
25	446.5	14.3	626	2 Q6DCH3	Q6dch3 xenopus lae
26	428.5	13.7	357	2 Q8SPW5	Q8spw5 macaca fasc
27	418.5	13.4	374	1 FCGL_HUMAN	FCGL_HUMAN
28	402.5	12.9	372	2 Q7YQJ5	Q7yqj5 canis fami
29	402.5	12.9	404	1 FCGL_MOUSE	FCGL_MOUSE
30	396	12.7	330	2 Q8R142	Q8r142 mus musculu
31	369	11.8	349	2 Q9MZT0	Q9mzt0 bos taurus

RESULT 1

Q96RD9 PRELIMINARY; PRT; 977 AA.
AC Q96RD9; DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Fc receptor-like protein 5.
GN Name=FCRH5;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396552; PubMed=11493702;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RT B cell expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777 (2001).
DR EMBL; AF397453; AAK93971.1; -
DR HSSP; PI2319; 1F2Q.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; IG; 8.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 8.
KW Receptor.
SQ SEQUENCE 977 AA; 106496 MW; 24EA4A027B25509E7 CRC64;

Query Match 94.4%; Score 2949; DB 2; Length 977;
Best Local Similarity 98.3%; Pred. No. 5e-204;
Matches 562; Conservative 2; Mismatches 4; Indels 4; Gaps 1;
QY 1 MLLWVLLVLPVSGQFARTPRPIIFLQPPWTVFQGERVLTCKGFRFYSPQTKWYHR 60
DB 1 MLLWVLLVLPVSGQFARTPRPIIFLQPPWTVFQGERVLTCKGFRFYSPQTKWYHR 60
QY 61 YLGEILLRETPDNLILEVQESGEYCOAGSPVHLDFSSASLILOAPLSVFEQDSVY 120
DB 61 YLGEILLRETPDNLILEVQESGEYCOAGSPVHLDFSSASLILOAPLSVFEQDSVY 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHACLKNDGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHACLKNDGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEEFTFPLRASSFQISGNPVTLTCEQSLERSDVLPRFPFDDDTLGLGWS 240
DB 181 VKIQVQEEFTFPLRASSFQISGNPVTLTCEQSLERSDVLPRFPFDDDTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGFWCKAATMPHSVSDSPRSWIQVQIPASHEVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFWCKAATMPHSVSDSPRSWIQVQIPASHEVLTLSPEKALNFE 300

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QY 301 GTKVTLHCETQEDSLRLTYRPFYHGVPLRHKSVCRCERGASISFSLTTENSGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRLTYRPFYHGVPLRHKSVCRCERGASISFSLTTENSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLI FEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLI FEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSHVPLTLSSA 480
DB 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSHVPLTLSSA 480
QY 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSTPSVGRVSFSLTEGHSNYY 540
QY 541 CTADNGFGPORSVSVLFTVKCKWLASKPPL 572
DB 541 CTADNGFGPORSVSVLFTVKCKWLASKPPL 572

RESULT 2
Q96LA4 PRELIMINARY; PRT; 734 AA.
AC Q96LA4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Fc receptor-like protein 3.
GN Name=FCRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RL B cell expression."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
DR EMBL; AY043466; AAKS1779.1; -.
DR HSSP; P12319; 1F2Q.
DR GO; GO:0004872; Fc receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 734 AA; 80827 MW; B359B494EBF12138 CRC64;

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Query Match 38.2%; Score 1193.5; DB 2; Length 734;
Best Local Similarity 45.5%; Pred. No. 1.9e-77;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPMTTVFQGERVTLTKGFRFVSPQ-KTKWYH 59
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPMTTVFQGERVTLTKGFRFVSPQ-KTKWYH 59
QY 60 RYLKKEILRETPDNILEVQESGEYRCQAQSPVLDLDFSSASLILQAPLSVFEQDSV 119
DB 60 RYLKKEILRETPDNILEVQESGEYRCQAQSPVLDLDFSSASLILQAPLSVFEQDSV 119
QY 61 ---DEKLKIKHKDKI-QITEPGNYQCKTRGSSLDVAHVFEFSPDWLILQALHPVFEQDNV 116
DB 61 ---DEKLKIKHKDKI-QITEPGNYQCKTRGSSLDVAHVFEFSPDWLILQALHPVFEQDNV 116
QY 120 VLRCRAKAEVTLNNTIYKNDNLVLAFLNKRTPDPIHACLDKNGAYRCTGVKESC---CPV 176
DB 120 VLRCRAKAEVTLNNTIYKNDNLVLAFLNKRTPDPIHACLDKNGAYRCTGVKESC---CPV 176
QY 177 SSNTVKIQVQEPFRPVLRASSQPIISGNPVTLTCTQLSLERSDVLPRFRFRDQTLG 236
DB 177 SSNTVKIQVQEPFRPVLRASSQPIISGNPVTLTCTQLSLERSDVLPRFRFRDQTLG 236

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DB 177 TSKPLNIQVQLFLHPLVLRASSSTPIEGSPMTLTCTQLSPQRPDVLQPSLFRDSQTLG 236
QY 237 LGWSLSPNFQITAMWSDSGFYWCKAATMHSVITSDSPRSWIOVQ-IPASHVTLTSPK 295
DB 237 LGWSLSPNFQITAMWSDSGFYWCKAATMHSVITSDSPRSWIOVQ-IPASHVTLTSPK 295
QY 237 LGWSRSPRLQIPAMWSDSGFYWCKAATMHSVITSDSPRSWIOVQ-IPASHVTLTSPK 295
DB 237 LGWSRSPRLQIPAMWSDSGFYWCKAATMHSVITSDSPRSWIOVQ-IPASHVTLTSPK 295
QY 296 ALNPEGTVTLHCEVORGSPQILYQFYHEDMPLVSSTPSVGRVSFSLTEGHSNYY 352
DB 296 ALNPEGTVTLHCEVORGSPQILYQFYHEDMPLVSSTPSVGRVSFSLTEGHSNYY 352
QY 353 YCTADNGLGAKPSKAVSLSVTPVSHVPLNLSPPEDLI FEGAKVTLHCEAQRGSLPILY 412
DB 353 YCTADNGLGAKPSKAVSLSVTPVSHVPLNLSPPEDLI FEGAKVTLHCEAQRGSLPILY 412
QY 412 YCTADNGLGAKPSKAVSLSVTPVSHVPLNLSPPEDLI FEGAKVTLHCEAQRGSLPILY 412
DB 412 YCTADNGLGAKPSKAVSLSVTPVSHVPLNLSPPEDLI FEGAKVTLHCEAQRGSLPILY 412
QY 413 QPHHEDALERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSH 472
DB 413 QPHHEDALERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSH 472
QY 416 RYFHEDVTLGNSSAPSGGASFNLSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSH 475
DB 416 RYFHEDVTLGNSSAPSGGASFNLSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSH 475
QY 473 PVLTLSSAEALTTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSTPSVGRVSFSLT 532
DB 473 PVLTLSSAEALTTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSTPSVGRVSFSLT 532
QY 476 PVLTLRAFGAQAQVVDLLELHCESLRGSFPILYFYHEDDTLGNISAHSGGASFNLSLT 535
DB 476 PVLTLRAFGAQAQVVDLLELHCESLRGSFPILYFYHEDDTLGNISAHSGGASFNLSLT 535
QY 533 EGHSGNYYCTADNGFGPORSVSVLFTVK 561
DB 533 EGHSGNYYCTADNGFGPORSVSVLFTVK 561
QY 536 TEHSGNYSCEADNGLGAQHSKVTNLNVTG 564
DB 536 TEHSGNYSCEADNGLGAQHSKVTNLNVTG 564

RESULT 3
Q96P31 PRELIMINARY; PRT; 734 AA.
AC Q96P31;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2a.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Xu M.-J., Zhao R., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416901; AAL3290.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 734 AA; 80855 MW; B3411B73A35EC668 CRC64;

Query Match 38.2%; Score 1193.5; DB 2; Length 734;
Best Local Similarity 45.5%; Pred. No. 1.9e-77;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPMTTVFQGERVTLTKGFRFVSPQ-KTKWYH 59
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPMTTVFQGERVTLTKGFRFVSPQ-KTKWYH 59
QY 60 RYLKKEILRETPDNILEVQESGEYRCQAQSPVLDLDFSSASLILQAPLSVFEQDSV 119
DB 60 RYLKKEILRETPDNILEVQESGEYRCQAQSPVLDLDFSSASLILQAPLSVFEQDSV 119
QY 61 ---DEKLKIKHKDKI-QITEPGNYQCKTRGSSLDVAHVFEFSPDWLILQALHPVFEQDNV 116
DB 61 ---DEKLKIKHKDKI-QITEPGNYQCKTRGSSLDVAHVFEFSPDWLILQALHPVFEQDNV 116
QY 120 VLRCRAKAEVTLNNTIYKNDNLVLAFLNKRTPDPIHACLDKNGAYRCTGVKESC---CPV 176
DB 120 VLRCRAKAEVTLNNTIYKNDNLVLAFLNKRTPDPIHACLDKNGAYRCTGVKESC---CPV 176
QY 177 SSNTVKIQVQEPFRPVLRASSQPIISGNPVTLTCTQLSLERSDVLPRFRFRDQTLG 236
DB 177 SSNTVKIQVQEPFRPVLRASSQPIISGNPVTLTCTQLSLERSDVLPRFRFRDQTLG 236

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QY 237 LGWSLSNFOITAMWSKDSGYFWCKAATMPHSVISDPSRWIQV-IPASHFVLTLSPEK 295
D 237 LGWSRSRLQIPAMWTDSSGYCEVETVTHSIKSLRSQIRVQRPVSNVNLIRPTG 296
QY 296 ALNPEGTVTLHCETQDSRLTYRFBHGVPPLRHKSVCRCASISFSLTT---ENSGN 352
D 297 GQLIEGENMVLICSAVAGSGTTFVSWHKEG-RVRSIGRKTQRLSLAEHLVLTVKESDAG 355
QY 353 YYCTADNGLGAKPSKAVSLVTPVSHPVNLNLSPEDLIEGAKVTLHCEAQRGSLPI 412
D 356 YYCAADNVHSPILSTWIRVTPVSHPVLTFRAPRAHTVVGDLLEHCESLRGSPPI 415
QY 413 QFHEDAALRRSANSAGGVAISFSLTAHSGNYCTADNGPQPSKAVSLITVPVSH 472
D 416 RFYHEDVTLGNSAPSGGASFNLSLTAHSGNYSCDADNGLGAQSHGVSLVTPVSR 475
QY 473 PVLTLSSAALTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSPVGRVSFSLT 532
D 476 PVLTRAPGAQAVVGDLLEHCESLRGSPPIYWFYHEDDTLGNISAHSGGASFNLSLT 535
QY 533 EHGSGNYCTADNGFGPQRSEVVSFLVTG 561
D 536 TEHSGNYSCEADNGLGAQSHKVTLNVTG 564

RESULT 4
Q8N6S2 PRELIMINARY; PRT; 742 AA.
AC Q8N6S2
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE FCRH3 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Scrausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC028933; AAH28933.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
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DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
SQ SEQUENCE 742 AA; 81853 MW; B06502007CAl9B8 CRC64;

Query Match 38.2%; Score 1193.5; DB 2; Length 742;
Best Local Similarity 45.5%; Pred. No. 1.9e-77;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFOGGRVTLTKGFRFYSPO-KTKVYH 59
D 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFOGGRVTLTKGFRFYSPO-KTKVYH 59
QY 60 RYLGEIILRETPDNILEQESGEYRCQAQGPLSPVHLDFFSSASLILQAFLSVFEGDSV 119
D 61 ----DKLLIKIKHDKI-QITEPGNYCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116
QY 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHPLACLKONGAYRCITGYKESC---CPV 176
D 117 ILRCQKDKNKHQKVVYKDKQLPNSYNLEKITYNSVSRDNSKYHCYAYRKFYILDIEV 176
QY 177 SNTVKIQVOEPFTRPVLRRASSFQIPSGNPVTLTCTETSLERSDVLPRFFRDRDQTLG 236
D 177 TSKPLNIQVQLFHPVLRASSSTPIEGSPMTLTCTETQLSPQRPDVLQFSLFRDSQTLG 236
QY 237 LGWSLSNFOITAMWSKDSGYFWCKAATMPHSVISDPSRWIQV-IPASHFVLTLSPEK 295
D 237 LGWSRSRLQIPAMWTDSSGYCEVETVTHSIKSLRSQIRVQRPVSNVNLIRPTG 296
QY 296 ALNPEGTVTLHCETQDSRLTYRFBHGVPPLRHKSVCRCASISFSLTT---ENSGN 352
D 297 GQLIEGENMVLICSAVAGSGTTFVSWHKEG-RVRSIGRKTQRLSLAEHLVLTVKESDAG 355
QY 353 YYCTADNGLGAKPSKAVSLVTPVSHPVNLNLSPEDLIEGAKVTLHCEAQRGSLPI 412
D 356 YYCAADNVHSPILSTWIRVTPVSHPVLTFRAPRAHTVVGDLLEHCESLRGSPPI 415
QY 413 QFHEDAALRRSANSAGGVAISFSLTAHSGNYCTADNGPQPSKAVSLITVPVSH 472
D 416 RFYHEDVTLGNSAPSGGASFNLSLTAHSGNYSCDADNGLGAQSHGVSLVTPVSR 475
QY 473 PVLTLSSAALTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSPVGRVSFSLT 532
D 476 PVLTRAPGAQAVVGDLLEHCESLRGSPPIYWFYHEDDTLGNISAHSGGASFNLSLT 535
QY 533 EHGSGNYCTADNGFGPQRSEVVSFLVTG 561
D 536 TEHSGNYSCEADNGLGAQSHKVTLNVTG 564

RESULT 5
Q96P29 PRELIMINARY; PRT; 740 AA.
AC Q96P29
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2c.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu M.-J., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF416903; AAL13292.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
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Qy	1	MLLVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRYSQ-KTKWYH	59
Db	1	MLLVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRYSQ-KTKWYH	60
Qy	60	RYLKGKELRTPNILEVQESGEYRCAQGSPLSSPVHLDFSSASLIQAPLSVFEQDSV	119
Db	61	---DEKLLKIKHDKI-QITEPGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV	116
Qy	120	VLCRAKAEVTLNNTIYK-NDNVLAFLNKRDTFPHIACLDKNGAYRCTGYKESC---	CPV 176
Db	117	ILRCQGDKNKNTHOKVYKDGKQLPNSYNLEKITVNSVSDNKKYHCTAYRKYVILDI	176
Qy	177	SSNTVKIQVCEFFRPV-----LRASSFQIPISGNPVTLTCEQLSLERSDVLPRFFR	230
Db	177	TSKZLNLOVQV---PVSNNLEIRPTGGQLIEGENVLI-C---SVAQSGGIVTWSHK	229
Qy	231	DDQTLGLG---WLSLSPNFQITAMWSKDSGFYWCKAATMPSHVSISDPSRWIQ--	VOIPA 284
Db	230	EGRVSLGRKTCQRLSLLAEHLVLTVKESDAGRYVCAADNVHSPILS-----	TWIRTVTRIPV 285
Qy	285	SHPVLTLSPEKALNFEGTKVTLHCETOEDSLRTLYRYHGVPLRHKSVCERCASISFS	344
Db	286	SHPVLTFRAPRAHTVWGDLELHCELSRGSPPIILYRYHEDVTLGNSAFSGGGAFNLS	345
Qy	345	LTENSNGNYCTADNGLCAKPSKAVSLSVTPVSHPVNLSSPEDLIFEAGKVTLHCEAQ	404
Db	346	LTAHSGNYSYCDADNGLGAQSHGVSLRVTPVSRPVLTLRAPGAQVWGDLLLEHCE	405
Qy	405	RGSLPILYQFHEDAAELRRSANGAGVAISFSLTAHSGNYYCTADNGFQPSKAVSL	464
Db	406	RGSPFILYFYHEDDTLGNISAHSGGASFNLSLTTEHSGNYSCEADNGLGAQSKRV	465
Qy	465	SIT-----VPVSHPVTLTSSAEALTFFEGATVTLHCEVQVQSGP	501
Db	466	NVTGTSRNRGLTAAGITGLVLSI-----LVLAALHLYVARARKP	508
RESULT 8			
ID	Q96PJ5	PRELIMINARY; PRT; 515 AA.	
AC	Q96PJ5	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	IFGP2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Tonsil;		
RX	MEDLINE=22033006; PubMed=12037601;		
RA	Guselnikov S.V., Eshova S.A., Mechetina L.V., Najakshin A.M.,		
RA	Volokva O.Y., Alabyev B.Y., Taranin A.V.;		
RT	"A family of highly diverse human and mouse genes structurally links		
RT	leukocyte FcR, gp42 and PECAM-1.";		
RL	Immunogenetics 54:87-95(2002).		
DR	EMBL; AF329490; AAL23900.1; -.		
DR	HSSP; P12319; IF2Q.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003598; IG_c2.		
DR	Pfam; PF00047; IG; 3.		
DR	SMART; SM00408; IGC2; 1.		
DR	PROSITE; P550835; IG_LIKE; 4.		
SQ	SEQUENCE 515 AA; 57224 MW; F3B7AD14FB1B449A CRC64;		
Query Match			
Best Local Similarity 26.5%; Score 826.5; DB 2; Length 515;			
Matches 184; Conservative 55; Mismatches 161; Indels 23; Gaps 6;			
Qy	1	MLLVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRYSQKTKWYH	60

Db	1	MLLVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRYSQKTKWYH	60
Qy	61	YLGKILRETPDNILEVQESGEYRCAQGSPLSPVHLDFSSASLIQAPLSVFEQDSV	120
Db	61	HWGKELTLPONTLEVRSSGLYRCAQGSFSPVRLFFSSDSLIQAPYSVFEQDLV	120
Qy	121	LRCRAKAEVTLNNTIYK-NDNVLAFLNKRDTFPHIACLDKNGAYRCTGYKESC	CPVSSN 179
Db	121	LRCHRRREKLTAVKYTWNGNLSKNSWDLIPQASSNNNGNYRCIGYDENDVFRSN	180
Qy	180	TVKIQVQEPFPTVLRASSFQIPISGNPVTLTCEQLSLERSDVLPRFFR	DDOTLGLW 239
Db	181	FKIIKIQELFPHPELKATDSQTEGNSVNLSCETQLPERSDTELFHFFRDGEVILSDW	240
Qy	240	SLSNPFQITAMWSKDSGFYWCKAATMPSHVSISDPSRWIQV-IPASHVTLTSP	PEKALN 298
Db	241	STYPELOLPTVWRENSGSGYWCAGTNRGNHKSPLQIHVQRPVSGVLTETOPSGQA	300
Qy	299	FGTKVTLHCETOEDSLRTLYRYHGV-PLRHKSVCERCASISFSLTTE	NSNYCT 356
Db	301	VEGEMLVLCVSAEGTGTTFSSHREDMQESLGRKTQSLRAELPAPROSHAGYICT	360
Qy	357	ADNGLCAKPSKAVSLSVTPVSHPVNLSSPEDLIFEAG-----KVTLHCEAQ	404
Db	361	ADNSYG--PVQSNVLNVTRTP-----GNRDLVAAGATGGLSALLAVALLP	HCWRR 413
Qy	405	RGS 407	
Db	414	RXS 416	
RESULT 9			
ID	Q96RE0	PRELIMINARY; PRT; 515 AA.	
AC	Q96RE0	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Fc receptor-like protein 4.		
GN	Name=FCRH4;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21395652; PubMed=11493702;		
RA	David R.S., Wang Y.H., Kubagawa H., Cooper M.D.;		
RA	"Identification of a family of Fc receptor homologs with preferential		
RT	B cell expression.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).		
DR	EMBL; AF397452; AAK93970.1; -.		
DR	HSSP; P12319; IF2Q.		
DR	GO; GO:0004872; Fc receptor activity; IEA.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003598; IG_c2.		
DR	Pfam; PF00047; IG; 3.		
DR	SMART; SM00408; IGC2; 1.		
DR	PROSITE; P550835; IG_LIKE; 4.		
KW	Receptor.		
SQ	SEQUENCE 515 AA; 57250 MW; 32FBD6FAB2B19D3D CRC64;		
Query Match			
Best Local Similarity 26.3%; Score 820.5; DB 2; Length 515;			
Matches 183; Conservative 55; Mismatches 162; Indels 23; Gaps 6;			
Qy	1	MLLVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRYSQKTKWYH	60
Db	1	MLLVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRYSQKTKWYH	60
Qy	61	YLGKILRETPDNILEVQESGEYRCAQGSPLSPVHLDFSSASLIQAPLSVFEQDSV	120

Db 61 HWGEKLTLPNTLVRESLYRCQARGSPRNPVLLFSSDSLLOQAPSYVPEGDTLV 120
 QY 121 LRCRAKAEVTLNNTYK-NDNLAFNLKRTDFHPIHACLKNDNGAYRTGYKESCCPVSSN 179
 Db 121 LRCRRRKEKLTAVKVTWNGNLSISNKSMDLLIPQASNNNGNYRCIGYGDENDVFLN 180
 QY 180 TVKIQVPEPFRPVLRASSFPISGNPVTLCETQLSLERSDYLPRFRFRDDOTLGLGW 239
 Db 181 FKIKIOELFPHPELKATDSOPTGNSVNLSCETQLPERSDPLPHNFFRDEGVLISDW 240
 QY 240 SLSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRSPSWIQV-IPASHPVLTLSPEKALN 298
 Db 241 STYPELQPLTVWRENSGSCYCAETVRGNIHKHSPSLQIHVQRIPVSGVLELTPQSGGQA 300
 QY 299 FEGKVTILHCBTQDSRLTYRFYHEGV--PLRHSVRCBGRGASISFSLTNSGNYICT 356
 Db 301 VEGEMLVLCVSAEGTGDITTFSHREDMQBSLGRKTORSURELELPAIRQSHAGGYCT 360
 QY 357 ADNGLGAKPKSAVSLSVTPVSHVNLNLSPPEDLIPEGA-----KVTILHCEAQ 404
 Db 361 ADNSYGV-PVQSVNLTVRETP-----GNRDGLVAAGATGGLLSALLAVALLFHCWRR 413
 QY 405 RGS 407
 Db 414 RKS 416

RESULT 10
 Q96LA5 PRELIMINARY; PRT: 508 AA.
 ID Q96LA5
 AC Q96LA5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fc receptor-like protein 2 (FcRH2).
 DE Name=FcRH2; ORFNames=UNQ9236;
 GN Name=FcRH2; ORFNames=UNQ9236;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 EN [1]
 RP SEQUENCE FROM N.A.
 RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
 RT "Identification of a family of Fc receptor homologs with preferential
 B cell expression.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22887296; PubMed=12975309;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; AY043465; AAK91778.1; -;
 DR EMBL; AY358130; AAQ88497.1; -;
 DR HSSP; P12319; 1F2Q.
 DR Genew; HGNC:14875; SPAP1.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 3.
 DR PROSITE; PS00835; IG_LIKE; 3.
 KW Receptor.
 SQ SEQUENCE 508 AA; 55541 MW; 9AB30E0411B41EDC CRC64;

Query Match 24.8%; Score 773.5; DB 2; Length 508;
 Best Local Similarity 47.3%; Pred. No. 2.4e-47;
 Matches 178; Conservative 46; Mismatches 137; Indels 15; Gaps 6;
 QY 104 SLILOAPLSVFEQDSVLRCAKAEVTLNNTYKNDN-VLAFLNKRTRDFHPIHACLKNDG 162
 Db 19 SLTLVAPSSVFEQDSVLRCAKAEVTLNNTYKNDN-VLAFLNKRTRDFHPIHACLKNDG 78
 QY 163 AYRC-TGYKESCCPVSSNTVQVQEPPTRPVLRASSFPISGNPVTLCETQLSLERSD 221
 Db 79 NYFCSTKGQLFLWMDKTSNIVKIQELFQRPVLTAASSFPQIEGGFVSLKCTRLSPQRLD 138
 QY 222 VPLRFRFRDDOTLGLHSLSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRSPSWIQV 281
 Db 139 VOLQCFRFRQVLSGWSSPPELOISAVSEDTGSYWCKAETVTHIRKQSLQSHVQ 198
 QY 282 -IPASHPVLTLSPEKALNFEKTKVTLHCETOEDSLRILYRFYHE--GVPLRHSVRCBGRG 338
 Db 199 RIPSINVSLEIRAPGGQVTEGOKLILCSVAGGTGNVTFWSYREATGTSMGKKTQR---- 254
 QY 339 ASISFSL-----TTNSGNYCYTADNGLGAKPKSAVSLSVTPVSHVNLNLSPPEDLIPE 393
 Db 255 -SLSAELIPAVKSDAGKYCRADNGHPVITQSKVNIPIVRIPVSRPVLTLRSPGAQAAV 313
 QY 394 GAKVTILHCEAQRGSLPILYQPHHEDALERRSANSAGVAISFSLTAHSGNYCYTADNNG 453
 Db 314 GDLLHCEALRGSPPILYQFYHEDVTLGNSSAFSGGASFNLSLTAHSGNYSCEANNG 373
 QY 454 FQPSKSAVSLSIIVP 469
 Db 374 LGAQCSEAVPVSISGP 389

RESULT 11
 AAQ88497 PRELIMINARY; PRT: 508 AA.
 ID AAQ88497
 AC AAQ88497;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE FCRH2
 GN UNQ9236.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 EN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=12975309;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
 Bioinformatics Assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; AY358130; AAQ88497.1; -;
 SQ SEQUENCE 508 AA; 55541 MW; 9AB30E0411B41EDC CRC64;

Query Match 24.8%; Score 773.5; DB 2; Length 508;
 Best Local Similarity 47.3%; Pred. No. 2.4e-47;
 Matches 178; Conservative 46; Mismatches 137; Indels 15; Gaps 6;
 QY 104 SLILOAPLSVFEQDSVLRCAKAEVTLNNTYKNDN-VLAFLNKRTRDFHPIHACLKNDG 162
 Db 19 SLTLVAPSSVFEQDSVLRCAKAEVTLNNTYKNDN-VLAFLNKRTRDFHPIHACLKNDG 78

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QY 163 AYRC-TGYKSCCPVSNVTKIOVQBPFRPVLRASSFOPIGPNVTLTCTQLSLERSD 221
Db 79 NYFCSTKQGLFLWDRKTSNIVKIKVQLFQRPVLTASSFOPIEGGPNVSLKCTELSPQLD 138
QY 222 VPLRFFPRDDQTLGLGWSLSPNFQITAWKSDGSPYWCATMPHSVLSDSFPRWIOVQ 281
Db 139 VQLOFCFFRQNLVSGWSSSPLOLSAYWSEDTGYNCKAETVTHIRKQSLQSQIHVQ 198
QY 282 -IPASHPVLTLSPEKALNPEGTAVTLHCETQEDSLTLRYFHE--GVPLRHKSVCRCRG 338
Db 199 RIPSINVSLEIRAPGQVTEGQKILLCSVAGTGNVTFWYEEAGTSMGKTKOR--- 254
QY 339 ASISFSL-----TTSNGNYCYCTADNGLGAKPSKAVSLSVTPVSHPVNLNLSPEDLIFE 393
Db 255 -SLSAELEIPAVKESDAGKYCYCRADNGHVPISQKVVNIPVRIEVSFVLTLSRSPGAQAAV 313
QY 394 GAKVTLHCEAQRSLPLTYOFHEDAALEERSANSAGGVAISPLTAHSGNYCYCTADNG 453
Db 314 GDLELHCEALRSPPLTYOFIYHEDVTLGNSSAPSGGASFNLSLTAHSGNYSCENANG 373
QY 454 FGORSKAVSLISITVP 469
Db 374 LGAQCSAEVPSISGP 389

RESULT 12
Q8N732 PRELIMINARY; PRT; 360 AA.
ID Q8N732;
AC Q8N732;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE DJ801G22.1 (Novel immunoglobulin domain protein similar to
immunoglobulin receptors) (Fragment).
GN Name=dJ801G22.1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RA Baguley C.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL135929; CAB92793.1; -.
DR HSSP; F12319; IFQ.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IGLIKE; 4.
KW Receptor.
FT NON_TER 1
FT NON_TER 360
FT NON_TER 360
SQ SEQUENCE 360 AA; 40724 MW; 7ACC2B7FA3256D62 CRC64;

Query Match 24.7%; Score 772; DB 2; Length 360;
Best Local Similarity 46.1%; Pred No. 2e-47;
Matches 165; Conservative 49; Mismatches 138; Indels 6; Gaps 4;

QY 22 RPIILQPPWTVFQGERVLTCKGFRFYPSPQTKWYHYLGKEILRTPNILEVQDSG 81
Db 4 KEVISHPPTWTFKXGERVLTCKNGFQFVATEKTTWYHRHWYGEKLTTPGNTLEVRSG 63
QY 82 EYRCQAGSPLSPVHLDPSSASLILOAPLSVFEGDSVYLRCAAEVTLNNTIYK-NDN 140
Db 64 LYRCQAGSPRENVELLFSSLSLILOAPLSVFEGDGLVLRCHRRKKEKLTAVKWTNGN 123
QY 141 VLAFLNKRDEIPIACILKDNCAVRCYTKYKSCCPVSNVTKIOVQBPFRPVLRASSFO 200
Db 124 ILSISNKSNDLLIPQASSNNNGYRCIGYGDENDVFRSFKIKIQLFPPHKLKATDSQ 183
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QY 201 PISGNVTLTCTQLSLERSDVLPRFRDDOTLGLGWSLSPNFQITAWKSDGSPYWC 260
Db 184 PTEGNSVNLSCETQLPPEPRTDLPHFNFRDGEVILSDWSTYPELQLPVTWRENSGSYWC 243
QY 261 KAAATMPHSVLSDSFPRWIOVQ-IPASHPVLTLSPEKALNPEGTAVTLHCETQEDSLTLY 319
Db 244 GAETVRGNIHKHSPSLQIHVQRIEVSGLVLETOPSGGQAVEGEMLVLCVSAEGTGDTTF 303
QY 320 RFYHEGV--PLRHKSVCRCGASFSFISITENSNNYCYCTADNGLGAKPSKAVSLSVTV 375
Db 304 SWHREDQESLGRKTKQSLRAELPAIROSHAGGYCYCTADNSYG--PVOSWVLNVTV 359

RESULT 13
Q8BJAS PRELIMINARY; PRT; 508 AA.
ID Q8BJAS;
AC Q8BJAS;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Mus musculus activated spleen cDNA, RIKEN full-length enriched
DE library, clone:F830015F10 product:weakly similar to SH2 DOMAIN-
DE CONTAINING PHOSPHATASE ANCHOR PROTEIN 1C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RA MEDLINE=99279253; PubMed=10349636;
RA Carninci P.; Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RA MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RA MEDLINE=20499374; PubMed=11042159;
RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.;
RA Kanno H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RA MEDLINE=20530913; PubMed=11076861;
RA Shibata K.; Itoh M.; Aizawa K.; Nagaoaka S.; Sasaki N.; Carninci P.;
RA Kanno H.; Akiyama J.; Nishi K.; Kusunai T.; Taehiro H.; Itoh M.;
RA Sumi N.; Ishii Y.; Nakamura S.; Hazama M.; Nishine T.; Kashiwagi K.;
RA Yamamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Harada A.;
RA Fujiwaki E.; Inoue K.; Togawa Y.; Izawa M.; Ohara E.; Watanabe M.;
RA Yoneda Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsura S.; Kawai J.;
RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP
```



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RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hangaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089756; BAC40954.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG LIKE; 4.
SQ SEQUENCE 508 AA; 56795 MW; 27774A4733A9443F CRC64;

Query Match 22.2%; Score 692.5; DB 2; Length 508;
Best Local Similarity 40.9%; Pred. No. 1.7e-41;
Matches 160; Conservative 63; Mismatches 131; Indels 37; Gaps 6;

QY 105 LILQAPLSVEGDSVWLRCRAKAEVTLNN-TIYNNDNLVLAFLNKRTPDFHIPHACLKDNGA 163
DB 31 LVLQAPPAVFEGDSVWLRCYAKKIEAETLTFYKDGKALFLHPQSSELYIHANLKDNGQ 90

QY 164 YRCTGYKESC--CPVSNNTKIQVQEPFTRPVLRASSFPQISGNPVLTCETQLSLERSD 221
DB 91 YKTSKKKWSFGSLTSTYTRVQVELFRPVLRLRPSHPIDGSPVTLTCQTLSAQKSD 150

QY 222 VPLRFPRFRDDQTLGLGWSLSPFOITAMWSKDSGFYKCAATWPHSVISDSRSPSIQVQ 281
DB 151 ARLOFCFRNLQLLGGSCRSSEPHIPAIVTESKRYQCKAETVNSQVRKQSTAFIIPVQ 210

QY 282 IPASHPVLTLSPEKALNFEGTKVTLHCETOEDSLRTLYRPHGVF-----LRH 330
DB 211 RASARFQTHIIPASKLVFEGQLLLNCV-----KGVPGLKFSWKYKMDLN 257

QY 331 KSVCEGASISPSLTEN--SGNYCTADNGLGAKPKSAVLSVTVPVSHVPLNLSPP 387
DB 258 KEYILKSSNAEFKISQVNSDAGEVHREATNRRSFVSAFPIITIKVPVSQVVLTLTG 317

QY 388 EDLIFEKAKVTLHCDAQRGSLPILYQFHEDAALERRSANSAGVAISFSLTAHSGNY 447
DB 318 KQALEGLMTLHCQSQRGSPCLYEPFFYENVSLGNSLILSGGAYFNFSMSTERSGNY 377

QY 448 CTADNGEGPQPSKAVLSI-----TVPVS 471
DB 378 CTADNGLGACQCEAIRISIFDMTKNSRVPWA 408

RESULT 14
Q8NF56 ID Q8NF56 PRELIMINARY; PRT; 437 AA.
AC Q8NF56;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FLJ00333 protein (Fragment).
GN Name=FLJ00333;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090423; BAC03404.1; -.
DR InterPro; IPR003599; IG-like.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS0835; IG LIKE; 3.
FT NON_TER 1
SQ SEQUENCE 437 AA; 46521 MW; F56DED36523E52CA CRC64;

Query Match 21.0%; Score 557.5; DB 2; Length 437;
Best Local Similarity 50.5%; Pred. No. 4.7e-39;
Matches 140; Conservative 29; Mismatches 101; Indels 7; Gaps 2;

QY 291 LSPKALNFEGTK-----VTLHCETOEDSLRTLYRPHGVFPLRHKSVCRCGASISFS 344
DB 24 LAPSPSGFPGAQAVVGDLLHCEAPRGSPPILYWFVHEDVTLGSSAPSGEASFNLS 83

QY 345 LTTNSGNYCTADNGLGAKPKSAVLSVTVPVSHVPLNLSPPDLIFEGAKVTLHCDAQ 404
DB 84 LTAHSGNYSCEANGLVAQHSDTISLSVIVFVSRLPILTRAPRAQAVVGDLLHCEAL 143

QY 405 RGSPLILYQFHEDAALERRSANSAGVAISFSLTAHSGNYCTADNGFGPQPSKAVSL 464
DB 144 RGSPPILYWFVHEDVTLGKISAPSGGASFNLSLTTHSGIYSCDANGLEAQSEWVTL 203

QY 465 SITVPVSHVPLTSSAEALTFEGATVTLHCVEQVSGPQILYQFVHEDMPLVSSSTPVG 524
DB 204 KVAVPVSRLPILTRAPGTHAAVGDLLHCEALRGSPPILYRPHFHDVTLGNRSPS-GG 262

QY 525 VSFSLTEGHSNGNYCTADNGFGPQPSKAVSLVTVG 561
DB 263 ASLNLSTLAHSGNYSCEADNGLGAQRSETVILYITG 299

RESULT 15
Q9EQY5 ID Q9EQY5 PRELIMINARY; PRT; 509 AA.
AC Q9EQY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MMAN-g protein precursor (IFGP2) (Mus musculus adult male diencephalon
DE cDNA, RIKEN full-length enriched library, clone:9310158F12
DE product:macrophage scavenger receptor 2, full insert sequence) (Mus
DE musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2810439C17 product:macrophage scavenger
DE receptor 2, full insert sequence).
GN Name=Msr2; Synonyms=MMAN-g;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yoshimoto M., Matsumoto K., Ukai Y., Kitamura K.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090423; BAC03404.1; -.
DR InterPro; IPR003599; IG-like.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS0835; IG LIKE; 3.
FT NON_TER 1
SQ SEQUENCE 437 AA; 46521 MW; F56DED36523E52CA CRC64;

Query Match 21.0%; Score 557.5; DB 2; Length 437;
Best Local Similarity 50.5%; Pred. No. 4.7e-39;
Matches 140; Conservative 29; Mismatches 101; Indels 7; Gaps 2;

QY 291 LSPKALNFEGTK-----VTLHCETOEDSLRTLYRPHGVFPLRHKSVCRCGASISFS 344
DB 24 LAPSPSGFPGAQAVVGDLLHCEAPRGSPPILYWFVHEDVTLGSSAPSGEASFNLS 83

QY 345 LTTNSGNYCTADNGLGAKPKSAVLSVTVPVSHVPLNLSPPDLIFEGAKVTLHCDAQ 404
DB 84 LTAHSGNYSCEANGLVAQHSDTISLSVIVFVSRLPILTRAPRAQAVVGDLLHCEAL 143

QY 405 RGSPLILYQFHEDAALERRSANSAGVAISFSLTAHSGNYCTADNGFGPQPSKAVSL 464
DB 144 RGSPPILYWFVHEDVTLGKISAPSGGASFNLSLTTHSGIYSCDANGLEAQSEWVTL 203

QY 465 SITVPVSHVPLTSSAEALTFEGATVTLHCVEQVSGPQILYQFVHEDMPLVSSSTPVG 524
DB 204 KVAVPVSRLPILTRAPGTHAAVGDLLHCEALRGSPPILYRPHFHDVTLGNRSPS-GG 262

QY 525 VSFSLTEGHSNGNYCTADNGFGPQPSKAVSLVTVG 561
DB 263 ASLNLSTLAHSGNYSCEADNGLGAQRSETVILYITG 299
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 11:21:45 ; Search time 154 Seconds
(without alignments)
1379.011 Million cell updates/sec

Title: US-09-724-254A-3
Perfect score: 3124
Sequence: 1 MLLWVILLVLPVSGQFART.....ABPSLTHSKFLALSSFLP 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1980s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3111	99.6	592	4 AAB82314	Aab82314 Human imm
2	3111	99.6	592	7 ADM35236	Adm35236 Human LY1
3	2950	94.4	759	4 AAB82313	Aab82313 Human imm
4	2950	94.4	759	7 ADM35235	Adm35235 Human LY1
5	2950	94.4	977	4 AAB82315	Aab82315 Human imm
6	2950	94.4	977	6 ABP97215	Abp97215 Tumour-as
7	2950	94.4	977	7 ADM35237	Adm35237 Human LY1
8	1193.5	38.2	582	6 ABU99155	Abu99155 Novel hum
9	1193.5	38.2	582	8 ADM93875	Adm93875 Human NOV
10	1193.5	38.2	707	7 ADM06089	Adm06089 Human pro
11	1193.5	38.2	734	4 AAB82316	Aab82316 Human imm
12	1193.5	38.2	734	7 ADM35238	Adm35238 Human LY1
13	1193.5	38.2	733	8 ADL06557	Adl06557 Human tum
14	1176	37.6	727	6 ABB84668	Abb84668 Human SEC
15	1150.5	36.8	554	7 ADF74336	Adf74336 Extracell
16	1150.5	36.8	717	7 ADF74337	Adf74337 Human FCR
17	1150.5	36.8	717	7 ADF74318	Adf74318 Human FCR
18	1120	35.9	222	5 ABP69283	Abp69283 Human pol
19	900	28.8	181	5 ABP51264	Abp51264 Human MDD
20	900	28.8	181	5 ABP51409	Abp51409 Human MDD
21	889.5	28.5	570	7 ADF74389	Adf74389 Murine Fc
22	889	28.5	468	7 ADF74391	Adf74391 Extracell
23	847.5	27.1	639	7 ADJ70604	Adj70604 Human rea
24	826.5	26.5	515	4 AAB82312	Aab82312 Human imm
25	826.5	26.5	515	5 ABB80608	Abb80608 Human spg

26	826.5	26.5	515	7 ADM35234	Adm35234 Human LY1
27	826.5	26.5	515	8 ADP18669	Adp18669 Human pro
28	826	26.4	167	6 ABP75420	Abp75420 Human sec
29	803.5	25.7	421	6 ABU99156	Abu99156 Novel hum
30	803.5	25.7	421	6 ABU99157	Abu99157 Novel hum
31	803.5	25.7	421	8 ADM93877	Adm93877 Human NOV
32	786.5	25.2	421	8 ABU99158	Abu99158 Novel hum
33	786.5	25.2	421	8 ADM93881	Adm93881 Human NOV
34	783.5	25.1	445	7 ADM35268	Adm35268 Human LY1
35	773.5	24.8	508	4 AAB82317	Aab82317 Human imm
36	773.5	24.8	508	7 ADM35239	Adm35239 Human LY1
37	773.5	24.8	508	7 ADM35264	Adm35264 Human LY1
38	773.5	24.8	508	8 ADF89715	Adf89715 Human can
39	773.5	24.8	508	8 ADL06539	Adl06539 Human tum
40	769.5	24.6	380	7 ADF74334	Adf74334 Extracell
41	769.5	24.6	489	7 ADF74316	Adf74316 Human FCR
42	745	23.8	406	8 ADM93879	Adm93879 Human NOV
43	729.5	23.4	327	5 ABP63021	Abp63021 Human pol
44	713	22.8	397	7 ADM35277	Adm35277 Human LY1
45	703	22.5	460	7 ADM35273	Adm35273 Human LY1

ALIGNMENTS

RESULT 1

AAB82314

ID AAB82314 standard; protein; 592 AA.

XX

AC AAB82314;

XX

DT 23-JUL-2001 (first entry)

XX

DE Human immunoglobulin receptor isoform IRTA2b.

XX

KW Immunoglobulin superfamily receptor translocation associated; IRTA;

KW IRTA2b; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;

KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.

OS Homo sapiens.

XX

FH Key

PT Peptide

PT Protein

FT Modified-site

FT Modified-site

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

Location/Qualifiers

1..15

/label= Signal_peptide

16..592

/label= Mature_protein

132..134

/note= "Asn is N-glycosylated"

383..385

/note= "Asn is N-glycosylated"

WO200138490-A2.

31-MAY-2001.

28-NOV-2000; 2000WO-US032403.

29-NOV-1999; 99US-0168151P.

(UYCO) UNIV COLUMBIA NEW YORK.

Dalla-Favera R;

WPI; 2001-365921/37.

N-PSDB; AAF30951.

New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor

Translocation Associated proteins, used to treat B cell malignancies

including lymphomas and multiple myeloma.

Claim 3; Fig 18B-1-18B-2; 72pp; English.

The present sequence is that of the novel human immunoglobulin receptor,

CC

immunoglobulin superfamily receptor translocation associated protein isoform 2b (IRTA2b), an FC receptor involved in the pathogenesis of lymphoma and melanoma. Efforts to identify genes involved in chromosomal aberrations affecting band Ig21 in multiple myeloma and B cell lymphoma led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding members of a novel subfamily of related receptors within the immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315). IRTA2b is a 592 amino acid glycoprotein, which diverges from IRTA2a at residue 560, extending for a further 32 residues, whose hydrophobicity suggest docking to the plasma membrane via a GPI anchor. The IRTA2 genes display a specific pattern of expression in mature B cells. IRTA2 is expressed in GC centrocytes and in perfollicular cells, which may include immunoblasts and memory cells. The invention provides IRTA nucleic acids and proteins, and antibodies directed to an epitope of an IRTA protein. Methods are claimed for: detecting a B cell malignancy comprising a Ig21 chromosomal rearrangement using a nucleic acid molecule that specifically hybridises with a unique sequence of human IRTA1-5; and treating a subject having a B cell cancer by administering an anti-IRTA antibody or an antisense oligonucleotide that specifically hybridises to IRTA mRNA so as to prevent overexpression of IRTA protein and hence to arrest cell growth or induce cell death of cancer cells expressing IRTA. The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma and follicular lymphoma. The B cell lymphoma is selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma

XX Sequence 592 AA;

Query Match 99.6%; Score 3111; DB 4; Length 592;
Best Local Similarity 99.7%; Pred. No. 3.6e-219;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLWVLLVLPVSGQGFARTPRPIIFLOPPWTVFQGERVTLCKGFRFSPQTKWYHR 60
DB 1 MLLWVLLVLPVSGQGFARTPRPIIFLOPPWTVFQGERVTLCKGFRFSPQTKWYHR 60

QY 61 YLGEILRETPDNLVEQSEGEYRCQAGSPVHLDFSSASLILQAPLSVFEQDSVV 120
DB 61 YLGEILRETPDNLVEQSEGEYRCQAGSPVHLDFSSASLILQAPLSVFEQDSVV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLPFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLPFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVQPFPTPLVRASSFQIPISGNPVTLCTQLSLERSDVPFLRFRFFDDQTLGLWS 240
DB 181 VKIQVQPFPTPLVRASSFQIPISGNPVTLCTQLSLERSDVPFLRFRFFDDQTLGLWS 240

QY 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSEKALNFE 300

QY 301 GTKVTLHCETQEDSLRTLYFYHGVPLRHKSVCRCGASISPSLTENSGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLYFYHGVPLRHKSVCRCGASISPSLTENSGNYCTADNG 360

QY 361 LGAKPSKAVSLSVTPVSHVPLNLSPEDLIFEGAKVTLHCEAQRGSLPLIYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHVPLNLSPEDLIFEGAKVTLHCEAQRGSLPLIYQFHEDAA 420

QY 421 LERRSANSAGVAISFSLTAEHSGNYCTADNGFGFQORSKAVSLSTVPVSHPVLTLSSA 480
DB 421 LERRSANSAGVAISFSLTAEHSGNYCTADNGFGFQORSKAVSLSTVPVSHPVLTLSSA 480

QY 481 EALTTFEGATVTLHCEVQSGFQILYQFYHEDMPLVSSSTPSVGRVFSFSLTEGHSGNY 540
DB 481 EALTTFEGATVTLHCEVQSGFQILYQFYHEDMPLVSSSTPSVGRVFSFSLTEGHSGNY 540

QY 541 CTADNGFGPQSRSEVSVLFTVGKQWLASPKPLAEFSLTHSFKNLFASSFLP 592
DB 541 CTADNGFGPQSRSEVSVLFTVGKQWLASPKPLAEFSLTHSFKNLFASSFLP 592

RESULT 2

ADM35236
ID ADM35236 standard; protein; 592 AA.

XX ADM35236;

XX 03-JUN-2004 (first entry)

DE Human LY1448P cancer related protein for cancer detection method.

KW cytostatic; T-cell vaccine; detection; cancer;

KW chronic lymphocytic leukemia.

XX Homo sapiens.

XX WO2003077836-A2.

XX 25-SEP-2003.

XX 06-NOV-2002; 2002WO-US035728.

XX 06-NOV-2001; 2001US-C0040862.

XX 23-MAY-2002; 2002US-C0154884.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Retter M;

XX WPI; 2003-756941/71.

PT Detecting cancer in a patient comprises contacting a biological sample from the patient with a binding agent that binds to a cancer-associated polypeptide and comparing the amount of polypeptide to a predetermined cutoff value.

XX Disclosure; SEQ ID NO 10461; 419pp; English.

XX The invention relates to a method of detecting (M1) cancer in a patient by: (i) contacting a biological sample from the patient with an agent that binds to any of three polypeptides given in the specification; (ii) detecting in a sample an amount of the peptide that binds to the binding agent; and (iii) comparing the amount of polypeptide present in the patient's sample to a predetermined cutoff value. The specification also discloses a separate method for detecting (M2) cancer in a patient by a method similar to M1, except that the detection agent is an oligonucleotide that binds to any of three polynucleotides given in the specification. M1 and M2 are useful for detecting the presence of cancer in a patient, especially chronic lymphocytic leukemia. The applicants have identified specific human polypeptides overexpressed in one or more types of hematological malignancies. This sequence corresponds to a protein used in the method of the invention.

XX Sequence 592 AA;

Query Match 99.6%; Score 3111; DB 7; Length 592;
Best Local Similarity 99.7%; Pred. No. 3.6e-219;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLWVLLVLPVSGQGFARTPRPIIFLOPPWTVFQGERVTLCKGFRFSPQTKWYHR 60

DB 1 MLLWVLLVLPVSGQGFARTPRPIIFLOPPWTVFQGERVTLCKGFRFSPQTKWYHR 60

QY 61 YLGEILRETPDNLVEQSEGEYRCQAGSPVHLDFSSASLILQAPLSVFEQDSVV 120

DB 61 YLGEILRETPDNLVEQSEGEYRCQAGSPVHLDFSSASLILQAPLSVFEQDSVV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLPFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180

DB 121 LRCRAKAEVTLNNTIYKNDNVLPFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVQPFPTPLVRASSFQIPISGNPVTLCTQLSLERSDVPFLRFRFFDDQTLGLWS 240

Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQLSLERSDVLRRFRFRDDQTLGLWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPSHVSIDSFRSNIQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPSHVSIDSFRSNIQVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETOEDSLRILYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETOEDSLRILYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYOFHHEDAA 420
Db 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYOFHHEDAA 420
Qy 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLISITVPVSHPVLTLSA 480
Db 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLISITVPVSHPVLTLSA 480
Qy 481 EALTFEGATVTLHCEVQSGPQIILYQFYHEDMPLVSSSTPSVGRVSFSLTGHSGNYY 540
Db 481 EALTFEGATVTLHCEVQSGPQIILYQFYHEDMPLVSSSTPSVGRVSFSLTGHSGNYY 540
Qy 541 CTADNGFGPQRSSEVSVLFTVTKCWLASKPLAEFSLTHSFKNLFASSFLP 592
Db 541 CTADNGFGPQRSSEVSVLFTVTKCWLASHPLAEFSLTHSFKNLFASSFLP 592
RESULT 3
AA82313
ID AA82313 standard; protein; 759 AA.
XX AC AA82313;
XX DT 23-JUL-2001 (first entry)
XX DE Human immunoglobulin receptor isoform IRTA2a.
XX KW Immunoglobulin superfamily receptor translocation associated; IRTA;
KW IRTA2a; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FH Peptide 1..15
FT /label= Signal_peptide
FT Protein 16..759
FT /label= Mature_protein
FT Modified-site 132..134
FT /note= "Asn is N-glycosylated"
FT Modified-site 383..385
FT /note= "Asn is N-glycosylated"
FT Modified-site 621..623
FT /note= "Asn is N-glycosylated"
FT Modified-site 631..633
FT /note= "Asn is N-glycosylated"
FT Modified-site 714..716
FT /note= "Asn is N-glycosylated"
XX WO200138490-A2.
XX PN
XX PD
XX 31-MAY-2001.
XX PF 28-NOV-2000; 2000WO-US032403.
XX PR 29-NOV-1999; 99US-0168151P.
XX PA (UYCO) UNIV COLUMBIA NEW YORK.
XX PI Dalla-Favera R;
XX WPI; 2001-355921/37..
DR

DR N-PSDB; AAF30950.
XX New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor
PT Translocation Associated proteins, used to treat B cell malignancies
PT including lymphomas and multiple myeloma.
XX Claim 3; Fig 18B-1-18B-2; 72pp; English.
XX The present sequence is that of the novel human immunoglobulin receptor,
CC immunoglobulin superfamily receptor translocation associated protein
CC isoform 2a (IRTA2a), an Fc receptor involved in the pathogenesis of
CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal
CC aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma
CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
CC members of a novel subfamily of related receptors within the
CC immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA
CC isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315).
CC IRTA2a is a 759 amino acid secreted glycoprotein with 8 Ig-type domains
CC followed by a unique C-terminus. IRTA2b diverges from IRTA2a at residue
CC 560, extending for a further 32 residues. IRTA2c diverges from IRTA2a at
CC residue 746 and extends for a further 231 residues. The IRTA genes
CC display a specific pattern of expression in mature B cells. IRTA2 is
CC expressed in GC centrocytes and in perifollicular cells, which may
CC include immunoblasts and memory cells. The invention provides IRTA
CC nucleic acids and proteins, and antibodies directed to an epitope of an
CC IRTA protein. Methods are claimed for: detecting a B cell malignancy
CC comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule
CC that specifically hybridises with a unique sequence of human IRTA1-5; and
CC treating a subject having a B cell cancer by administering an anti-IRTA
CC antibody or an antisense oligonucleotide that specifically hybridises to
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,
CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-
CC Hodgkin's lymphoma
XX
SQ Sequence 759 AA;
Query Match 94.4%; Score 2950; DB 4; Length 759;
Best Local Similarity 98.4%; Pred. No. 3.2e-207;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLPQPPWTVTFQGERVTLTKGFRFYSQKTKWYHR 60
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLPQPPWTVTFQGERVTLTKGFRFYSQKTKWYHR 60
Qy 61 YLQKEILRETDPNILEVQESGEYRCOAQSPSSPVHLDPSSASLILQAPLSVFEQDSVV 120
Db 61 YLQKEILRETDPNILEVQESGEYRCOAQSPSSPVHLDPSSASLILQAPLSVFEQDSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPIHACLKDNAGYRCTGYKSCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPIHACLKDNAGYRCTGYKSCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQLSLERSDVLRRFRFRDDQTLGLWS 240
Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQLSLERSDVLRRFRFRDDQTLGLWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPSHVSIDSFRSNIQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPSHVSIDSFRSNIQVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETOEDSLRILYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETOEDSLRILYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYOFHHEDAA 420
Db 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYOFHHEDAA 420
Qy 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLISITVPVSHPVLTLSA 480

```
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVLSITVPVSHFVLTLSA 480
Qy 481 BALTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEHSGNYY 540
Db 481 BALTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEHSGNYY 540
Qy 541 CTADNGFGPORSSEVVSFLVTKGCVLASKPPL 572
Db 541 CTADNGFGPORSSEVVSFLVTKGCVLASKPPL 568

RESULT 4
ADM35235
ID ADM35235 standard; protein; 759 AA.
XX
AC ADM35235;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human LY1448P cancer related protein for cancer detection method.
XX
KW cytostatic; T-cell vaccine; detection; cancer;
XX
KW chronic lymphocytic leukemia.
XX
OS Homo sapiens.
XX
FN WO2003077836-A2.
XX
PD 25-SEP-2003.
XX
PF 06-NOV-2002; 2002WO-US035728.
XX
PR 06-NOV-2001; 2001US-00040862.
XX
PR 23-MAY-2002; 2002US-00154884.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Algate PA, Mannion J, Retter M;
XX
DR WPI; 2003-756941/71.
XX
PT Detecting cancer in a patient comprises contacting a biological sample
PT from the patient with a binding agent that binds to a cancer-associated
PT polypeptide and comparing the amount of polypeptide to a predetermined
PT cutoff value.
XX
PS Disclosure; SEQ ID NO 10460; 419pp; English.
XX
CC The invention relates to a method of detecting (M1) cancer in a patient
CC by: (i) contacting a biological sample from the patient with an agent
CC that binds to any of three polypeptides given in the specification; (ii)
CC detecting in a sample an amount of the peptide that binds to the binding
CC agent; and (iii) comparing the amount of polypeptide present in the
CC patient's sample to a predetermined cutoff value. The specification also
CC discloses a separate method for detecting (M2) cancer in a patient by a
CC method similar to M1, except that the detection agent is an
CC oligonucleotide that binds to any of three polynucleotides given in the
CC specification. M1 and M2 are useful for detecting the presence of cancer
CC in a patient, especially chronic lymphocytic leukemia. The applicants
CC have identified specific human polypeptides overexpressed in one or more
CC types of hematological malignancies. This sequence corresponds to a
CC protein used in the method of the invention.
XX
SQ Sequence 759 AA;
XX
Query Match 94.4%; Score 2950; DB 7; Length 759;
Best Local Similarity 98.4%; Pred. No. 3.2e-207;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLPQPTWTFQGERVLTCKGFRFYSPOKTKWYR 60
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLPQPTWTFQGERVLTCKGFRFYSPOKTKWYR 60
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Qy 61 YLGKEILRETNDNILEVQESGEYRCQAGSPVHLDFSSASLILQAPLSVFEQSVV 120
Db 61 YLGKEILRETNDNILEVQESGEYRCQAGSPVHLDFSSASLILQAPLSVFEQSVV 120
Qy 121 LRCRAKAVTLNNTIYKNDNVLAFLNKRTDPhiPACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAVTLNNTIYKNDNVLAFLNKRTDPhiPACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFQPIISGNPVTLCETQLSLERSDVPRLRFRFRDDQTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFQPIISGNPVTLCETQLSLERSDVPRLRFRFRDDQTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCKAATNPHSVISDSPRSMIOVOIPASHVPLTILSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCKAATNPHSVISDSPRSMIOVOIPASHVPLTILSPEKALNFE 300
Qy 301 GTKVTLHCETOEDSLRTLYRFYHGVPLRHKSVCERGASISFSLTTEHSGNYCTADNG 360
Db 301 GTKVTLHCETOEDSLRTLYRFYHGVPLRHKSVCERGASISFSLTTEHSGNYCTADNG 360
Qy 361 LGAKPSKAVLSVTVPVSHPVNLSSPEDLIFEGAKVTLHCEAORGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVLSVTVPVSHPVNLSSPEDLIFEGAKVTLHCEAORGSLPILYQFHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVLSITVPVSHFVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVLSITVPVSHFVLTLSA 480
Qy 481 BALTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEHSGNYY 540
Db 481 BALTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEHSGNYY 540
Qy 541 CTADNGFGPORSSEVVSFLVTKGCVLASKPPL 572
Db 541 CTADNGFGPORSSEVVSFLVTKGCVLASKPPL 568

RESULT 5
AAB82315
ID AAB82315 standard; protein; 977 AA.
XX
AC AAB82315;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human immunoglobulin receptor isoform INTA2c.
XX
KW Immunoglobulin superfamily receptor translocation associated; IRTA;
KW IRTA2c; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FT Peptide 1..15
FT Protein 16..977
FT Modified-site 132..134
FT Modified-site 383..385
FT Modified-site 621..623
FT Modified-site 631..633
FT Modified-site 714..716
FT Modified-site 795..797
FT Modified-site 806..808
FT Modified-site 806..808
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Modified-site	816..818 /note= "Asn is N-glycosylated"	
Modified-site	843..845 /note= "Asn is N-glycosylated"	
Domain	851..873 /note= "transmembrane domain"	
Binding-site	899..902 /note= "putative consensus Src-homology 2 (SH2) binding domain"	
Binding-site	924..927 /note= "putative consensus Src-homology 2 (SH2) binding domain"	
Binding-site	954..957 /note= "putative consensus Src-homology 2 (SH2) binding domain"	
WO200138490-A2.		
31-MAY-2001.		
28-NOV-2000; 2000WO-US032403.		
29-NOV-1999; 99US-0168151P.		
(UYCO) UNIV COLUMBIA NEW YORK.		
Dalla-Favera R;		
WPI; 2001-355921/37.		
N-PSDB; AAF30952.		
New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor Translocation Associated proteins, used to treat B cell malignancies including lymphomas and multiple myeloma.		
Claim 3; Fig 1B3-1-1B3-2; 72pp; English.		
The present sequence is that of the novel human immunoglobulin receptor.		

CC isoform 2C (IRTA2c), an FC receptor involved in the pathogenesis of
CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal
CC aberrations affecting band Iq21 in multiple myeloma and B cell lymphoma
CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
CC members of a novel subfamily of related receptors within the
CC immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA
CC isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82313 and AAB82314).
CC IRTA2c is the longest isoform. It is a type I transmembrane glycoprotein.
CC Each SH2 binding site agrees with the immune receptor tyrosine-based
CC inhibition motif (ITIM) consensus and is encoded by a separate exon. The
CC IRTA genes display a specific pattern of expression in mature B cells.
CC IRTA2 is expressed in GC centrocytes and in perifollicular cells, which
CC may include immunoblasts and memory cells. The invention provides IRTA
CC nucleic acids and proteins, and antibodies directed to epitopes of IRTA
CC proteins. Methods are claimed for detecting a B cell malignancy
CC comprising a Iq21 chromosomal rearrangement using a nucleic acid molecule
CC that specifically hybridises with a unique sequence of human IRTA1-5; and
CC treating a subject having a B cell cancer by administering an anti-IRTA
CC antibody or an antisense oligonucleotide that specifically hybridises to
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,
CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-
CC Hodgkin's lymphoma

XX Sequence 977 AA;

Query Match 94.4%; Score 2950; DB 4; Length 977;
Best Local Similarity 98.4%; Pred. No. 4.4e-207;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QV 1 MLIIWILLVLAPVSGOFARTPRPIIFLOQPWTIVTQGERVILTKGFRFSPQKTKYHR 60

Db 241 LSPNFQITAMWSKDSGYWYCAATMPHSVLSDSRSHIQVOIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETQEDSLRLTYRHYEGVPLRHKSVCRCRGASISPSLTSTNSGNYYCTADNG 360
Db 301 GTKVTLHCETQEDSLRLTYRHYEGVPLRHKSVCRCRGASISPSLTSTNSGNYYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHVPLNLSPEDLIFSGAKVTLHCRCAGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSPEDLIFSGAKVTLHCRCAGSLPILYQFHEDAA 420
Qy 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLISITVPVSHVPLTSSA 480
Db 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLISITVPVSHVPLTSSA 480
Qy 481 EALTPEGATVTLHCRCAGSLPILYQFHEDMPLVSSSTPSVGRVSPFSLTTEGHSNYY 540
Db 481 EALTPEGATVTLHCRCAGSLPILYQFHEDMPLVSSSTPSVGRVSPFSLTTEGHSNYY 540
Qy 541 CTADNGFGPQRSSEVVSFLVTGKCVLASKPPL 572
Db 541 CTADNGFGPQRSSEVVSFLVTGKCVLASKPPL 572
RESULT 8
ID ABU99155 standard; protein; 582 AA.
XX AC ABU99155;
XX DT 01-AUG-2003 (first entry)
XX DE Novel human GPCR related protein NOV17a.
XX Human; G-protein coupled receptor related protein; GPCR related protein;
KW NOV; cytostatic; cardiant; antiarteriosclerotic; antidiabetic;
KW immunomodulator; anti-HIV; anorectic; antisthmatic; haemostatic;
KW antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine;
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;
KW diabetes; immune disorder; AIDS; obesity; asthma;
KW haematopoietic disorder; Parkinson's disease; Alzheimer's disease;
KW infection; multiple sclerosis; cancer-associated cachexia;
KW wasting disorder; chronic disease; neurogenesis; cell differentiation;
KW cell proliferation; haematopoiesis; wound healing; angiogenesis;
KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.
XX OS Homo sapiens.
XX WO200299116-A2.
XX PD 12-DEC-2002.
XX PF 04-JUN-2002; 2002WO-US017428.
XX PR 04-JUN-2001; 2001US-0295607P.
XX PR 04-JUN-2001; 2001US-0295661P.
XX PR 06-JUN-2001; 2001US-0296404P.
XX PR 06-JUN-2001; 2001US-0296418P.
XX PR 14-JUN-2001; 2001US-0296285P.
XX PR 15-JUN-2001; 2001US-0298556P.
XX PR 21-JUN-2001; 2001US-029949P.
XX PR 26-JUN-2001; 2001US-0300883P.
XX PR 28-JUN-2001; 2001US-0301550P.
XX PR 13-AUG-2001; 2001US-0311972P.
XX PR 27-AUG-2001; 2001US-0315071P.
XX PR 29-AUG-2001; 2001US-0315660P.
XX PR 14-SEP-2001; 2001US-0322293P.
XX PR 17-SEP-2001; 2001US-0322706P.
XX PR 14-DEC-2001; 2001US-0341186P.
XX PR 28-FEB-2002; 2002US-0361189P.
XX PR 12-MAR-2002; 2002US-0363673P.
XX PR 12-MAR-2002; 2002US-0363676P.
XX PR 03-JUN-2002; 2002US-00363676.

PA (CURA-) CURAGEN CORP.
XX Anderson DW, Baumgartner JC, Boldog EL, Casman SJ, Edinger SR;
PI Ganguli EA, Gerlach VL, Gorman L, Guo X, Hjalte T, Kekuda R, Li L;
PI MacDougall JR, Malyankar UM, Millet I, Padigaru M, Patturajan M;
PI Pena CE, Rastelli L, Shimkets RA, Stone DJ, Spytek KA, Vernet CM;
PI Voss EZ, Zerhusen BD;
XX WPI: 2003-140627/13.
DR N-PSDB; ACD03659.
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX Claim 1; Page 166; 332pp; English.
XX The invention describes an isolated polypeptide (I) comprising any of 27
CC 118-961 residue amino acid sequences, given in the specification, a
CC mature form of them, a sequence that is at least 95 % identical to them,
CC or a sequence having one or more conservative substitutions in them. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease selected from a pathology
CC associated with the polypeptide. The NOVX polypeptides, polynucleotides
CC and antibodies are useful in treating or preventing NOVX-associated
CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune
CC disease, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's
CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer-
CC associated cachexia, and other wasting disorders associated with chronic
CC diseases. The nucleic acids and polypeptides may also be used as targets
CC for the identification of small molecules that modulate or inhibit e.g.
CC neurogenesis, cell differentiation, cell proliferation, haematopoiesis,
CC wound healing and angiogenesis, in gene therapy, in generation of
CC antibodies that bind immunospecifically to NOVX substances for use in
CC therapeutic or diagnostic methods. The nucleic acids are further used as
CC hybridisation probes in chromosome mapping, tissue typing, preventive
CC medicine, and pharmacogenomics. The polypeptides are also useful as
CC vaccines. This is the amino acid sequence of a novel human G-protein
CC coupled receptor related protein NOV
XX Sequence 582 AA;
Query Match 38.2%; Score 1193.5; DB 6; Length 582;
Best Local Similarity 45.5%; Pred. No. 1.1e-78;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;
Qy 1 MLMLVILLVAVSGQFARTPRPIIFLPPTVTFQGERVTLTCGFRYSQ-KTKVNH 59
Db 1 MLMLVILLVAVSGQFARTPRPIIFLPPTVTFQGERVTLTCGFRYSQ-KTKVNH 59
Qy 60 RYLGKILRETDPNILEVQESGEYRCQAGSPVHLDSSASILCAPLSVPEGDSV 119
Db 60 RYLGKILRETDPNILEVQESGEYRCQAGSPVHLDSSASILCAPLSVPEGDSV 119
Qy 61 ---DEKLLIKKHDKI-QITEPGNYQCKTRGSSLSDDAHVVEFDPDWLLQALHPVEGDV 116
Db 61 ---DEKLLIKKHDKI-QITEPGNYQCKTRGSSLSDDAHVVEFDPDWLLQALHPVEGDV 116
Qy 120 VLRCRAKAEVTLNNTYKNDNVLAFLNKRTPHICHLKNDGAYECTGYKESC---CPV 176
Db 120 VLRCRAKAEVTLNNTYKNDNVLAFLNKRTPHICHLKNDGAYECTGYKESC---CPV 176
Qy 117 ILRCQKDNKNTVHKYKDGKLPNSYNLEKTVNSVRDNSKYHTAYRKYFLDIEV 176
Db 117 ILRCQKDNKNTVHKYKDGKLPNSYNLEKTVNSVRDNSKYHTAYRKYFLDIEV 176
Qy 177 SSNTVKIQVQEPTRPVLRRASSPQPTSGNPVTLTCTQLSLERSDYPLRFRFRDDDTLG 236
Db 177 SSNTVKIQVQEPTRPVLRRASSPQPTSGNPVTLTCTQLSLERSDYPLRFRFRDDDTLG 236
Qy 177 TSKPLNIQVQELFLHPVLRASSSTPIEGSPMTTCTQLSPQRPDVOLOFSLFRDSTLG 236
Db 177 TSKPLNIQVQELFLHPVLRASSSTPIEGSPMTTCTQLSPQRPDVOLOFSLFRDSTLG 236
Qy 237 LKWSLSNFOITAMWSKDSGYWYCAATMPHSVLSDSRSHIQVOIPASHPVLTLSPEK 295
Db 237 LKWSLSNFOITAMWSKDSGYWYCAATMPHSVLSDSRSHIQVOIPASHPVLTLSPEK 295
Qy 237 LGWSRSPRLQIPAMWTEDSGSYVCEVETVTHSKKSLRSQIRVQRPVSNVLEIRPTG 296
Db 237 LGWSRSPRLQIPAMWTEDSGSYVCEVETVTHSKKSLRSQIRVQRPVSNVLEIRPTG 296
Qy 296 ALNPEGTKVTLHCETQEDSLRLTYRHYEGVPLRHKSVCRCRGASISFSLT---ENSGN 352
Db 296 ALNPEGTKVTLHCETQEDSLRLTYRHYEGVPLRHKSVCRCRGASISFSLT---ENSGN 352
Qy 297 GQLIEGENVNLCSVAQSGTGTFSMHKEG-RVRSILGRKTRQSRLLAEHLVTLVKESDAGR 355
Db 297 GQLIEGENVNLCSVAQSGTGTGTFSMHKEG-RVRSILGRKTRQSRLLAEHLVTLVKESDAGR 355
Qy 353 YYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSPEDLIFEGAKVTLHCRCAGSLPILY 412
Db 353 YYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSPEDLIFEGAKVTLHCRCAGSLPILY 412

Db 356 YCAADNVHSPILSTWIRTVRI PVSHPVLTFRAPRAHTVVGDLELHCELSRGPILY 415
 QY 413 QFHEDAALEPERSANSAGGVAISLSLTAHSGNYCTADNGFGPQRSKAVSLSTVPSH 472
 Db 416 RYFHEDEVTLGNSSAPSGGASFNLSLTAHSGNYSCTADNGLGAGHSHGSLRVTVPSR 475
 QY 473 PVLTLSSAEALTFFGATVTLHCEVQRGSPQILYOFYHEDMPLVSSSTPSVGRVSFSPSLT 532
 Db 476 PVLTLRAGCAAVGDDLELHCELSRGSFPILYFHYHEDDTLGNISAHSGGASFNLSLT 535
 QY 533 EHGSGNYCTADNGFGPQRSVSLFTVG 561
 Db 536 TEHSGNYSCEADNGLGAGHSHKSVTLNVTG 564

RESULT 9
 ADM93875
 ID ADM93875 standard; protein; 582 AA.
 AC ADM93875;
 XX
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human NOV protein #47.
 XX
 KW gene therapy; vaccine; NOVX; cancer; neurodegenerative disorder;
 KW Parkinson's disease; metabolic disorder; diabetes; obesity;
 KW immune related disorder; tissue typing; human.
 XX Homo sapiens.
 XX
 FN US2004009480-A1.
 XX
 PD 15-JAN-2004.
 XX
 PF 03-JUN-2002; 2002US-00162335.
 XX
 PR 04-JUN-2001; 2001US-0295607P.
 PR 04-JUN-2001; 2001US-0295661P.
 PR 06-JUN-2001; 2001US-0296404P.
 PR 06-JUN-2001; 2001US-0296418P.
 PR 11-JUN-2001; 2001US-0297414P.
 PR 12-JUN-2001; 2001US-0297567P.
 PR 14-JUN-2001; 2001US-0298285P.
 PR 15-JUN-2001; 2001US-0298556P.
 PR 21-JUN-2001; 2001US-0299499P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 28-JUN-2001; 2001US-0301550P.
 PR 13-AUG-2001; 2001US-0311972P.
 PR 27-AUG-2001; 2001US-0315069P.
 PR 27-AUG-2001; 2001US-0315071P.
 PR 29-AUG-2001; 2001US-0315660P.
 PR 14-SEP-2001; 2001US-0322293P.
 PR 17-SEP-2001; 2001US-0322706P.
 PR 14-DEC-2001; 2001US-0341186P.
 PR 28-FEB-2002; 2002US-0361189P.
 PR 12-MAR-2002; 2002US-0363673P.
 PR 12-MAR-2002; 2002US-0363676P.
 XX
 (ANDE//) ANDERSON D W.
 (BAUM//) BAUMGARTNER J C.
 (BOLD//) BOLDOG F L.
 (CASM//) CASMAN S J.
 (EDIN//) EDINGER S R.
 (GANG//) GARGOLLI E A.
 (GERL//) GERLACH V.
 (GORM//) GORMAN L.
 (GUOX//) GUO X S.
 (HJAL//) HJALT T.
 (KEKU//) KEKUDA R.
 (LILL//) LI L.
 (MACD//) MACDOUGALL J R.
 (MALY//) MALYANKAR U M.

PA (MILL//) MILLET I.
 PA (PADI//) PADIGARU M.
 PA (PATI//) PATTURAJAN M.
 PA (PENA//) PENA C E A.
 PA (RAST//) RASTELLI L.
 PA (SHIM//) SHIMKETS R A.
 PA (STON//) STONE D J.
 PA (SPYT//) SPYTEK K A.
 PA (VERN//) VERNET C A M.
 PA (VOSS//) VOSS E Z.
 PA (ZERH//) ZERHUSEN B D.
 XX
 XX
 PI Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR,
 PI Gangolli EA, Gerlach V, Gorman L, Guo XS, Hjal T, Kekuda R, Li L,
 PI MacDougall JR, Malvankar UM, Millet I, Padigar M, Patturajan M,
 PI Pena CE, Rastelli L, Shimkets R, Stone DJ, Spytek KA, Vernet CM,
 PI Voss EZ, Zerhusen BD;
 XX WPI; 2004-090456/09.
 DR N-PSDB; ADM93874.
 XX
 PT New NOVX polypeptide, useful for preparing a composition for treating or
 PT preventing e.g., cancer, neurodegenerative disorders such as Parkinson's
 PT disease, or metabolic disorders such as diabetes or obesity, or for
 PT tissue typing.
 XX
 PS Claim 1; SEQ ID NO 94; 202pp; English.
 XX
 CC The invention relates to an isolated NOVX polypeptide. The polypeptide is
 CC useful for preparing a composition for treating or preventing a pathology
 CC associated with NOVX polypeptide e.g. cancer, neurodegenerative disorders
 CC such as Parkinson's disease, metabolic disorders such as diabetes or
 CC obesity or immune related disorders or for tissue typing. The present
 CC sequence represents a human NOV protein.
 XX
 SQ Sequence 582 AA;
 Query Match 38.2%; Score 1193.5; DB 8; Length 582;
 Best Local Similarity 45.5%; Pred. No. 1.1e-78;
 Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;
 QY 1 MLLAVILLVLPVSGQFARTPRPIIFQPPWTTVFQSERVTLCTCKGRFFYSPO-KTWYH 59
 Db 1 MLLWLLLLILTPGREQSGVAPKAVLLNPPWSTAFKGEKVALICSSISHSLAQGDITYH 60
 QY 60 RYLKHEILRETPDNILEVOESGEYRCQAQSPVHLDPFSSASLIQAPLSVFEQSDV 119
 Db 61 ---DEKLLIKHKDKI-QITEFGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116
 QY 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFHPACLKDNAGYRCTGYKESC---CPV 176
 Db 117 ILRCQKDNKTHOKVYKDGKQLPNSVLEKIVNSVRDNKXKHTARKFILLIEV 176
 QY 177 SSNTVKIQVBPPTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVPFRFRFFDDQTLG 236
 Db 177 TSKPLNIQVBLFLHPVLRASSSTPIEGSPMTLTCTQLSPQRPDVQLQSLFRDQTLG 236
 QY 237 LGWSLSNFOITAMKSKDSGYMCKAATMPHSHVSDSPRWIQVQ-IPASHPVLTLSPEK 295
 Db 237 LGWSRSPRLQIPAMWTEDSGVSWEVETVTHSIKGRLSRQIRVQRPVSNVNLEIRPTG 296
 QY 296 ALNFEGRKTVLHCETQBDLSLTLRYFHYHGVLPRLKSVRCERGASISFSLTT---ENSGN 352
 Db 297 GQLIEGENWVLICVAQSGGVTVTFSMHKEG-RVRSUGRKTRQSLLAELHVLTVKESDAGR 355
 QY 353 YYCTADNGLGAKPSKAVSLSTVPSVHPVNLNSPEDLIPEGKVTLLHCAQSRSLDILY 412
 Db 356 YYCAADNVHSPILSTWIRTVRI PVSHPVLTFRAPRAHTVVGDLELHCELSRGPILY 415
 QY 413 QFHEDAALEPERSANSAGGVAISLSLTAHSGNYSCTADNGFGPQRSKAVSLSTVPSH 472
 Db 416 RYFHEDEVTLGNSSAPSGGASFNLSLTAHSGNYSCTADNGLGAGHSHGSLRVTVPSR 475

QY 473 PVLTLSSAEALTFEGATVTLHCEVQSGPQLLYQFYHEDMPLVSSSTPVGVRVSFSLT 532
Db 476 PVLTLAPGAQAVGVGDLLEHCESLRGSPFIYWFYHEDDTLGNISAHSGGASFNLSLT 535
QY 533 EGHSGNYCTADNGFGPQSEVSLFVTG 561
Db 536 TEHSGNYSCADNGLGAQHSKVTLNVTG 564

RESULT 10
ID ADM06089 standard; protein; 707 AA.
XX
AC ADM06089;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein of the invention SEQ ID NO:4774.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.
XX
PN EPI347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yanamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI: 2003-723558/69.
DR N-PSDB; ADM03646.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 4774; 305pp; English.
XX
XX The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 707 AA;

Query Match 38.2%; Score 1193.5; DB 7; Length 707;
Best Local Similarity 45.5%; Pred. No. 1.5e-78;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;
QY 1 MLLWVLLVLPVSGQFARTPRPIIFLPQPTWTFVQGERVLTCKGFFYSQ-KTKMYH 59
Db 1 MLLWVLLVLTGREGSGVAPKAVLLNPPWSTAFKGEKVALICSSISHSLAQGDYVYH 60
QY 60 RVLGHEILRETPDNLVEQSEYRCQAGSPVHLDPSASLILOQLSVFEGDSV 119
Db 61 ---DEKLKIKHDKI-QTEPGNYQCKRGSLSDAVHVEFSPDWLIIQALHPFEGDNV 116
QY 120 VLRCRAKAEVTLNNIYKNDNLVAFLNKRTDFPHIACLKONGAYRCGTGYKESC---CPV 176

Db 117 ILRCGGKDNKNTKQVYVYKDGKQLPNYSNLEKITVNSVRDNSKYHCTAYRKFIYLDIEV 176
QY 177 SSNTVKIQVQPPFPVLRASSPQIPISGNPVTLTCETQLSLERSDVLRRFRFRDDOTLG 236
Db 177 TSKPLNIQVQELFLHPVLRASSSTPIEGSPMTLTCETQLSPQRPDVQLQSLFRDSQTLG 236
QY 237 LGWSLSPNFOITAMWSKDSGFYWCKAATMPHSVISDSPRSIVQV-IPASHPVLTLSPEK 295
Db 237 LGWSRSPKLIQIPAMWTEDSGSYWCVEVTVTHSIKKRSLRSQIRVQRPVPSNVNLEIRPTG 296
QY 296 ALNFEPTKVTLHCEVQSGPQLLYQFYHEDMPLVSSSTPVGVRVSFSLT---ENSGN 352
Db 297 GQLIEGENNVLICVAQSGGTVTFSWHKEG-RVRSGLRKTQSRLLAEHLVTLVSKESDAGR 355
QY 353 YYCTADNGLGAKPKSKAVSLSVTPVSHPVLLNLSPEDLIFEGAKVTLHCEAQRGLPILY 412
Db 356 YYCAADNVHSPILSTWIRVTVRIPVSHPVLTFRAPRAHTVVGDLLEHCESLRGSPPIY 415
QY 413 QPHHEDAAALERRSANSAGVAISFSLTAHSGNYCTADNGFGPQSEVSLFVTG 472
Db 416 RPYHEDVTLGNSSAPSGGGASFNLSLTAHSGNYSCADNGLGAQHSKVTLNVTG 475
QY 473 PVLTLSSAEALTFEGATVTLHCEVQSGPQLLYQFYHEDMPLVSSSTPVGVRVSFSLT 532
Db 476 PVLTLAPGAQAVGVGDLLEHCESLRGSPFIYWFYHEDDTLGNISAHSGGASFNLSLT 535
QY 533 EGHSGNYCTADNGFGPQSEVSLFVTG 561
Db 536 TEHSGNYSCADNGLGAQHSKVTLNVTG 564

RESULT 11
ID AAB82316 standard; protein; 734 AA.
XX
AC AAB82316;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human immunoglobulin receptor IRTA3 protein.
XX
KW Immunoglobulin superfamily receptor translocation associated; IRTA3;
KW human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma; myeloma;
KW B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO2001138490-A2.
XX
PD 31-MAY-2001.
XX
PF 28-NOV-2000; 2000WO-US032403.
XX
PR 29-NOV-1999; 99US-0168151P.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Dalla-Favera R;
XX
DR WPI: 2001-355921/37.
DR N-PSDB; AAF30953.
XX
PT New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor
PT Translocation Associated proteins, used to treat B cell malignancies
PT including lymphomas and multiple myeloma.
XX
PS Claim 4; Fig 18C-1-18C-2; 72pp; English.
XX
XX The present sequence is that of the novel human immunoglobulin receptor,
CC immunoglobulin superfamily receptor translocation associated protein 3
CC (IRTA3), an Fc receptor involved in the pathogenesis of lymphoma and
CC melanoma. Efforts to identify genes involved in chromosomal aberrations
CC affecting band 1q21 in multiple myeloma and B cell lymphoma led to the

CC discovery of IRTA1 and IRTA2 (see AAB82312-15) as founding members of a
 CC novel subfamily of related receptors within the immunoreceptor family. 3
 CC Additional proteins, IRTA3, IRTA4 and IRTA5 (see AAB82316-18), were
 CC subsequently identified, which are also members of this novel subfamily.
 CC The IRTA genes display a specific pattern of expression in mature B
 CC cells. IRTA3 is expressed in GC centrocytes and in perifollicular cells,
 CC which may include lymphoblasts and memory cells. This is analogous to
 CC IRTA2 expression. The invention provides IRTA nucleic acids and proteins,
 CC and antibodies directed to an epitope of an IRTA protein. Methods are
 CC claimed for: detecting a B cell malignancy comprising a Ig21 chromosomal
 CC rearrangement using a nucleic acid molecule that specifically hybridises
 CC with a unique sequence of human IRTA1-5; and treating a subject having a
 CC B cell cancer by administering an anti-IRTA antibody or an antisense
 CC oligonucleotide that specifically hybridises to IRTA mRNA so as to
 CC prevent overexpression of IRTA protein and hence to arrest cell growth or
 CC induce cell death of cancer cells expressing IRTA. The B cell cancer is
 CC selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma,
 CC Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma
 CC and follicular lymphoma. The B cell lymphoma is selected from mucosa-
 CC associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma
 CC
 XX Sequence 734 AA;
 SQ
 Query Match 38.2%; Score 1193.5; DB 4; Length 734;
 Best Local Similarity 45.5%; Pred. No. 1.5e-78;
 Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;
 QY 1 MLLVILLVLAPVSGQFARTPRPIIFLOPWTTFVQGERVTLCKGFRFYSPQ-KTKWYH 59
 Db 1 MLLVILLVLTPGREGQGVAPKAVLLNPPWSTAFKGEKVALICSSISHSLAQGDITYWH 60
 QY 60 RYLCKEILRETPDNLIVQSGEYRCQAQSPSSPVHLDFFSASLILQAPLSVFGDSV 119
 Db 61 ---DEKLLIKHDKI-QITEFGNYQCKTRGSSLSDAVHVFSPDWLILQALHPVFGDNV 116
 QY 120 VLRCRAAEVTLNNTIYKNDNLAFNLKRTDFHPIHACLKDNKAYRGTGKESK---CPV 176
 Db 117 ILRCQKDNKNTQKVVYKDGKQLPNSYNLEKITVNSVSRDNSKYHCTAYRKFYLDIEV 176
 QY 177 SSNTVKIQVQEPFTRPVLRASSQPTSGNPNVTTCETQLSLERSDVLPRFRDDOQTLG 236
 Db 177 TSKPLNIQVQLFLHPVLRASSSTPIEGSPMTLTCTQLSPQPDVQLQSLFRDSQTLG 236
 QY 237 LGWLSLNFQITAMWSKDSGFYCKAATMPHSVLSDSRSMIOVO-IPASHPVLTLSPEK 295
 Db 237 LGWRSRPLQIPAMWTEDSGSYWCEVETVTHSIKRSLSRQIRVQRPVSNVNLIRPTG 296
 QY 296 ALNFEQTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVRCERCAISFSLTT---ENSGN 352
 Db 297 GQLTEGENMVLICSAVQSGTTFVSMHKEG-RVRSGLRKTQRLSLLAEHLVLTVKESDAGR 355
 QY 353 YVCTADNGLGAKSKAVSLVTPVSHVPLNLSPEDLIPEGAKVTLHCEAQRGSPILLY 412
 Db 356 YVCAADNVHSPILSTWTRVTRIPVSHPVLTFRAPRAHTVVGDLLEHCELSRGSPILY 415
 QY 413 QFHEDAAALRRSANSAGGVAISFSLTAHSGNYYCTADNGFQQRKAVSLISITVPVSH 472
 Db 416 RFYHEDVTLGNSSAFSGGASFNLSLTAHSGNYSADADNGLCAQSHGSLRVTPVSR 475
 QY 473 PVLTLSABEALTPEGATVTLHCEVQRGSPQILYQFTHEDMPLVSSSTPVGVSFSLT 532
 Db 476 PVLTLPAGQAQVVDGDLLEHCELSRGSPFILIYFWYHEDDTLGNISAHSGGASFNLSLT 535
 QY 533 EGHSGNYCTADNGFGQPRGEVSLFVTG 561
 Db 536 TERSGNYSCEADNGLGQHSKVTNLNTG 564
 RESULT 12
 ADM35238
 ID ADM35238 standard; protein; 734 AA.
 XX
 AC ADM35238;

XX 03-JUN-2004 (first entry)
 XX Human LY1448P cancer related protein for cancer detection method.
 DE cytostatic; T-cell vaccine; detection; cancer;
 KW chronic lymphocytic leukemia.
 XX Homo sapiens.
 XX WO2003077936-A2.
 XX 25-SEP-2003.
 XX 06-NOV-2002; 2002WO-US035728.
 PR 06-NOV-2001; 2001US-00040962.
 PR 23-MAY-2002; 2002US-00154884.
 XX (CORI-) CORIXA CORP.
 XX Gaiger A, Algate PA, Mannion J, Retter M;
 XX WPI; 2003-756941/71.
 DR Detecting cancer in a patient comprises contacting a biological sample
 XX from the patient with a binding agent that binds to a cancer-associated
 PT polypeptide and comparing the amount of polypeptide to a predetermined
 PT cutoff value.
 XX
 PS Disclosure; SEQ ID NO 10463; 419pp; English.
 XX
 CC The invention relates to a method of detecting (M1) cancer in a patient
 CC by: (i) contacting a biological sample from the patient with an agent
 CC that binds to any of three polypeptides given in the specification; (ii)
 CC detecting in a sample an amount of the peptide that binds to the binding
 CC agent; and (iii) comparing the amount of polypeptide present in the
 CC patient's sample to a predetermined cutoff value. The specification also
 CC discloses a separate method for detecting (M2) cancer in a patient by a
 CC method similar to M1, except that the detection agent is an
 CC oligonucleotide that binds to any of three polynucleotides given in the
 CC specification. M1 and M2 are useful for detecting the presence of cancer
 CC in a patient, especially chronic lymphocytic leukemia. The applicants
 CC have identified specific human polypeptides overexpressed in one or more
 CC types of hematological malignancies. This sequence corresponds to a
 CC protein used in the method of the invention.
 XX
 SQ Sequence 734 AA;
 Query Match 38.2%; Score 1193.5; DB 7; Length 734;
 Best Local Similarity 45.5%; Pred. No. 1.5e-78;
 Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;
 QY 1 MLLVILLVLAPVSGQFARTPRPIIFLOPWTTFVQGERVTLCKGFRFYSPQ-KTKWYH 59
 Db 1 MLLVILLVLTPGREGQGVAPKAVLLNPPWSTAFKGEKVALICSSISHSLAQGDITYWH 60
 QY 60 RYLCKEILRETPDNLIVQSGEYRCQAQSPSSPVHLDFFSASLILQAPLSVFGDSV 119
 Db 61 ---DEKLLIKHDKI-QITEFGNYQCKTRGSSLSDAVHVFSPDWLILQALHPVFGDNV 116
 QY 120 VLRCRAAEVTLNNTIYKNDNLAFNLKRTDFHPIHACLKDNKAYRGTGKESK---CPV 176
 Db 117 ILRCQKDNKNTQKVVYKDGKQLPNSYNLEKITVNSVSRDNSKYHCTAYRKFYLDIEV 176
 QY 177 SSNTVKIQVQEPFTRPVLRASSQPTSGNPNVTTCETQLSLERSDVLPRFRDDOQTLG 236
 Db 177 TSKPLNIQVQLFLHPVLRASSSTPIEGSPMTLTCTQLSPQPDVQLQSLFRDSQTLG 236
 QY 237 LGWLSLNFQITAMWSKDSGFYCKAATMPHSVLSDSRSMIOVO-IPASHPVLTLSPEK 295
 Db 237 LGWRSRPLQIPAMWTEDSGSYWCEVETVTHSIKRSLSRQIRVQRPVSNVNLIRPTG 296

QY 296 ALNPEGKVTLHCETQEDSLRTLYRFVHEGVPLRHKSVMRCGASISFSLTT---ENSGN 352
Db 297 GQLIEGNNVLICSVAGSGTTFVSHKKG-RVRSGLRKTQRLSLAEHLVLTVKESDAGR 355
QY 353 YYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSSPEDLIFEGAKVTLHCEAQRGSPLILY 412
Db 356 YYCAADNVHSPILSTWIRVTRIPVSHFVLTRAPRAHTVVGDLLEHLCESLRGSPILY 415
QY 413 QFHEDDAALERRSANSAGGVAISFSLTAHSGNYCYTADNGFGPORSKAVSLSVTPVSH 472
Db 416 RFVHEDVTLGNSAPSGGGASFNLSLTAHSGNYSCTADNGLGAQSHGVSLRVTPVSR 475
QY 473 PVLTLSSAEALTPEGAFTLHCEVQSGPQILYQFVHEDMPLVSSSTPSPVGRVVSFSLT 532
Db 476 PVLTLRPAQAQVVGDLLEHLCESLRGSPILYWFYHEDDTLGNISAHSGGGASFNLSLT 535
QY 533 EGHSGNYCYTADNGFGPORSVSLFVTG 561
Db 536 TEHSGNYSCEADNGLGAQSHKVTLNVTG 564

RESULT 13

ADL06557
ID ADL06557 standard; protein; 733 AA.
XX AC ADL06557;
XX XX
XX 20-MAY-2004 (first entry)
XX DE Human tumour-associated antigenic target (TAT) polypeptide #56.
XX XX Human; tumour-associated antigenic target; TAT; cell death; tumour;
XX KW cancer; cytostatic.
XX OS Homo sapiens.
XX XX
XX PN WO2004016225-A2.
XX PD 26-FEB-2004.
XX PF 19-AUG-2003; 2003WO-US025892.
XX PR 19-AUG-2002; 2002US-0404809P.
XX PR 21-AUG-2002; 2002US-0405645P.
XX PR 23-SEP-2002; 2002US-0413192P.
XX PR 15-OCT-2002; 2002US-0419008P.
XX PR 15-NOV-2002; 2002US-0426847P.
XX PR 02-JUL-2003; 2003US-0484959P.
XX PA (GETH) GENENTECH INC.
XX PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
XX PI Spencer SD, Wu TD, Zhang Z;
XX XX
XX DR WPI: 2004-257144/24.
XX DR N-PSDB: ADL06478.

XX PS New antibody that binds to a tumor-associated antigenic target (TAT)
XX PT polypeptide, useful for preparing a composition for diagnosing or
XX PT treating cancer.
XX XX
XX PS Claim 2; SEQ ID NO 137; 319pp; English.
XX CC The present invention relates to the isolation of human tumour-associated
XX CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
XX CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
XX CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
XX CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
XX CC produced in bacteria or in CHO cells and induces death of a cell to which
XX CC it binds. The antibody is useful for preparing a composition for
XX CC diagnosing or treating tumours and cancer. The present sequence
XX CC represents a human TAT polypeptide of the invention.

Seq Sequence 733 AA;
Query Match 38.1%; Score 1191; DB 8; Length 733;
Best Local Similarity 45.3%; Pred. No. 2.3e-78;
Matches 258; Conservative 77; Mismatches 220; Indels 14; Gaps 7;
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGRFFYSPQ-KTKWYH 59
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGRFFYSPQ-KTKWYH 60
QY 60 RVLGKEILRETPDNILVEQESGEVRCOAGSPLSPVHLDFFSSASLILQAPLSVFEQDSV 119
Db 61 ---DEKLKIKHD--IQITFQNGVCKTRGSSLDADAVHVSFDWLLILQALHPVFEQDNV 115
QY 120 VLRCRAKAEVLTNNITYKNDVLAFLNKRITDFHPLACLKNGAYRCTGYKESC---CPV 176
Db 116 LLRCQCKDNKTHQKVVYKDGKQLPNSYNLEKITVNSVRDNSKYHCTAYRKFYILDIEV 175
QY 177 SNTVKIQOEBPTPRVLRASSFOPISGNPVLTLCETOLSLERSDVPRLRFFRDDQTLG 236
Db 176 TSKPLNIQVELFHPVLRASSTPIEGSPMLTLCETQLSPQRPDVQLOSLFRDSQTLG 235
QY 237 LGWSLSPNPQITAMWSKDSGFYWCATMPSHVSIDSPPRSWIQV-IPASHPLVLTLSPEK 295
Db 236 LGWSRSPRLQIPAMWTEDSGSYKCEVETVTHSIKXSLRSQIRVQRPVPSNVNLEIRPTG 295
QY 296 ALNFEGTKVTLHCETQEDSLRTLYRFVHEGVPLRHKSVMRCGASISFSLTT---ENSGN 352
Db 296 GQLIEGNNVLICSVAGSGTTFVSHKKG-RVRSGLRKTQRLSLAEHLVLTVKESDAGR 354
QY 353 YYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSSPEDLIFEGAKVTLHCEAQRGSPLILY 412
Db 355 YYCAADNVHSPILSTWIRVTRIPVSHFVLTRAPRAHTVVGDLLEHLCESLRGSPILY 414
QY 413 QFHEDDAALERRSANSAGGVAISFSLTAHSGNYCYTADNGFGPORSKAVSLSVTPVSH 472
Db 415 RFVHEDVTLGNSAPSGGGASFNLSLTAHSGNYSCTADNGLGAQSHGVSLRVTPVSR 474
QY 473 PVLTLSSAEALTPEGAFTLHCEVQSGPQILYQFVHEDMPLVSSSTPSPVGRVVSFSLT 532
Db 476 PVLTLRPAQAQVVGDLLEHLCESLRGSPILYWFYHEDDTLGNISAHSGGGASFNLSLT 534
QY 533 EGHSGNYCYTADNGFGPORSVSLFVTG 561
Db 535 TEHSGNYSCEADNGLGAQSHKVTLNVTG 563
RESULT 14
ABB84668
ID ABB84668 standard; protein; 727 AA.
XX AC ABB84668;
XX DT 11-FEB-2003 (first entry)
XX DE Human SECP-20 protein from clone 8039739CD1 SEQ ID 20.
XX XX
XX KW Secreted protein; SECP; human; antiarteriosclerotic; antiatherosclerotic;
XX KW hepatotropic; cytostatic; anti-HIV; antiallergic; antiasthmatic; cancer;
XX KW antianemic; antidiabetic; antiinflammatory; neuroprotective; antiulcer;
XX KW antithumatic; antiarthritic; cardiac; hypotensive; gonadal dysgenesis;
XX KW vasotropic; anticonvulsant; nootropic; immunosuppressive; pericarditis;
XX KW antiparkinsonian; ophthalmological; cell proliferative disorder;
XX KW arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; angina pectoris;
XX KW autoimmune disorder; AIDS; Crohn's disease; multiple sclerosis; epilepsy;
XX KW ulcerative colitis; cardiovascular disorder; myocardial infarction;
XX KW Raynaud's disease; myocarditis; neurological disorder; cataract;
XX KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
XX KW developmental disorder; Duchenne muscular dystrophy; antipsoriatic;
XX KW Becker muscular dystrophy; Cushing's syndrome.
XX OS Homo sapiens.
XX XX

PN WO200279441-A2.
 XX 10-OCT-2002.
 XX 29-MAR-2002; 2002WO-US009820.
 XX 30-MAR-2001; 2001US-0280527P.
 PR 06-APR-2001; 2001US-0282112P.
 PR 09-APR-2001; 2001US-0282702P.
 PR 13-APR-2001; 2001US-0283855P.
 PR 19-OCT-2001; 2001US-0343718P.
 PR 07-DEC-2001; 2001US-0339236P.
 PR 13-FEB-2002; 2002US-0357002P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Baughn MR, Burford N, Ding L, Duggan BM, Elliott VS, Forsythe J;
 PI Gandhi AR, Gietzen KJ, Griffin JA, He A, Honchell CD, Ison CH;
 PI Lal PG, Lee EA, Lee S, Lu DAM, Mason PM, Sanjanwala MM;
 PI Swarnakar A, Rankumar J, Tang YT, Thangavelu K, Tran UK, Walla NK;
 PI Warren BA, Yao MG, Xu Y, Yue H;
 XX WPI; 2003-058429/05.
 DR N-ESDB; ABS57564.
 XX Novel human secreted protein useful for treating, preventing or
 PT diagnosing cancer, hepatitis, psoriasis, asthma, diabetes mellitus,
 PT anemia, epilepsy, cataract, Alzheimer's disease.
 XX Claim 75; Page 165-166; 188pp; English.
 XX This invention describes novel secreted proteins (SECP) which have
 CC anti-atherosclerotic, anti-atherosclerotic, hepatotropic, cytostatic, anti
 CC -HIV, anti-allergic, anti-asthmatic, anti-anemic, anti-diabetic,
 CC anti-inflammatory, neuroprotective, anti-ulcer, anti-psoriatic, vasotropic,
 CC anti-rheumatic, anti-arthritis, cardiac, hypotensive, anticonvulsant,
 CC nootropic, immunosuppressive, anti-parkinsonian and ophthalmological
 CC activity. The polynucleotides and polypeptides of the invention can be
 CC used for diagnosing, treating or preventing cell proliferative disorder
 CC e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, cancer,
 CC autoimmune/inflammatory disorders e.g. acquired immunodeficiency syndrome
 CC (AIDS), allergies, asthma, anaemia, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, ulcerative colitis, psoriasis, rheumatoid arthritis,
 CC etc; cardiovascular disorder e.g. myocardial infarction, angina pectoris,
 CC hypertension, Raynaud's disease, myocarditis, pericarditis, etc;
 CC neurological disorders e.g. epilepsy, Huntington's disease, Parkinson's
 CC disease, Alzheimer's disease, Creutzfeldt-Jakob disease, etc; and
 CC developmental disorders e.g. Duchenne and Becker muscular dystrophy,
 CC cataract, gonadal dysgenesis, Cushing's syndrome, etc. The products of
 CC the invention can also be used for drug screening, proteome analysis,
 CC microarrays creating knock-in humanised animals or transgenic animals to
 CC model human diseases, in somatic or germline gene therapy, to generate a
 CC transcript image of a tissue or cell type, for detecting differences in
 CC the chromosomal location due to translocation, inversion, etc., among
 CC normal, carrier or affected individuals, and as hybridization probes for
 CC mapping naturally occurring genomic sequences. ABS84649-ABS84673
 CC represent secreted proteins disclosed by the cDNA's shown in ABS57545-
 CC ABS57569, described in the disclosure of the invention
 XX Sequence 727 AA;
 SQ
 Query Match 37,68; Score 1176; DB 6; Length 727;
 Best Local Similarity 45,28; Pred No. 2.9e-77;
 Matches 257; Conservative 76; Mismatches 216; Indels 20; Gaps 8;
 Qy 1 MLLWVLLVAPVSGQFARTPRIFIQPPTWTFQGERVTLKGRFRYSPO-KTKWYH 59
 Db 1 MLLWVLLVAPVSGQFARTPRIFIQPPTWTFQGERVTLKGRFRYSPO-KTKWYH 53
 Qy 60 RYLKGETILRETPNILEVQSGEVRCAQSGPLSSPVHLDFSSASLILQAPLSVREGDSV 119
 Db 54 ---DEKLUKIKHDKI-QITSPGNVQCKTRGSSUSDAVHVEFSPDWLILQALHPVFEQDNV 109

QY 120 VLRCEAKAEVTLNNTIYKNDVLAFLNKRTPHFLPACLDKNGAYRCTGYKESC---CPV 176
 Db 110 ILRCQKDNKNTKHKYVYKQKGLPNNSYNLEKITVSVSRDNSKYHCTAKRKFIILIEV 169
 QY 177 SSNTVKIQVQEPFTRPVLRASSFQISGNPVTLTCTQLSLERSDVPRLFRFFRDDQTLG 236
 Db 170 TSKPLNIQVQELFLHPVLRASSSTPIEGSPMTLCTQLSPQRPDVQLQFSLFRDSQTLG 229
 QY 237 LQWSLSPNFQITAMWSDGPFYCKAATPHSVISDSPRSWIQV-IPASHPVLTLSPEK 295
 Db 230 LQWSRSPRLQIPAMWTEDSGYSWCEVETVTHSIKRLSRQIRVQRFVSVNVNLEIRPTG 289
 QY 296 ALNPEGTVKTLHCETOEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSJTT---ENSGN 352
 Db 290 GQLEGENWVLCVAGQSGTTFVSMHKEG-RVSLGRKTOESLLAEHLVLTVKESDAGR 348
 QY 353 YYCTADNGLGAKPKAVSLSVTVVSHPVVLNLSPEDLIFEGAKVTLHCEAQRGSLPILY 412
 Db 349 YYCAADNVHSPILSTWIRTVIRIPVSHPVLTFRAPRAHTVVGDLELHCESLRGSPPILY 408
 QY 413 QPHHEDAALERRSANSAGGVAISFSLTAHSGNYYCTADNCGFGQFQSKAVSLSTIVPVSH 472
 Db 409 RPYHEDVTLGNSSAPSGGASFNLSLTAHSGNVCDAADNGLGAQHSHGVSLRTVTVSVR 468
 QY 473 PVLTLSSAEALTFFEGAVTLHCEVQVQSGPQILYQFYHEDMPLVSSSTPVSQVRSFSLT 532
 Db 469 PVLTLRAPGAQVAVGDLELHCESLRGSFPILYWFYHEDDTLGNISAHSGGASFNLSLT 528
 QY 533 EGHSGNYYCTADNCGFGQVQSGSEVSLFVTG 561
 Db 529 TEHSGNVCDAADNGLGAQHSHGVSLRTVTVSVR 557
 RESULT 15
 ADF74336
 ID ADF74336 standard; protein; 554 AA.
 AC ADF74336;
 DT 26-FEB-2004 (first entry)
 XX Extracellular domain of the human FcRH3 protein (SeqID 24).
 DE Fc receptor homologue; FcRH; human; chromosome 1q21-23;
 XX type I transmembrane receptor; immunoglobulin; cellular immunity;
 KW haematopoietic cell lineage; inflammatory; autoimmune disease;
 KW humoral immune response; anti-inflammatory; immunosuppressive.
 OS Homo sapiens.
 XX WO2003089624-A2.
 PN 30-OCT-2003.
 PD 25-MAR-2003; 2003WO-US009600.
 PF 25-MAR-2002; 2002US-0367667P.
 PR (UABR-) UAB RES FOUND.
 XX Davis RS, Cooper MD;
 PI WPI; 2003-854118/79.
 DR New isolated Fc receptor homologue (FcRH) comprising a cytoplasmic,
 PT transmembrane and an extracellular region, useful for the diagnosis
 PT and/or treatment of hematopoietic cell lineage, inflammatory and
 PT autoimmune diseases.
 XX Claim 30; SEQ ID NO 24; 135pp; English.
 PS This invention relates to novel members of the Fc receptor homologue
 CC (FcRH) subfamily mapped to human chromosome 1q21-23, as well as fragments

CC and variants thereof. Specifically, it refers to the type I transmembrane
CC receptors for the Fc region of immunoglobulins and the alternatively
CC spliced homologues, which work to modulate cellular and humoral immunity.
CC The present invention indicates that each FcRH has an extracellular
CC region, a transmembrane region and cytoplasmic region, where the latter
CC comprises one or more immunoreceptor tyrosine-based inhibitory or
CC activation motifs. As such, the methods and compositions described herein
CC are useful for the diagnosis and/or treatment of haematopoietic cell
CC lineage, inflammatory and autoimmune diseases, as well as in the
CC modulation of a humoral immune response in a subject. Accordingly, these
CC compositions have antiinflammatory and immunosuppressive activities. This
CC polypeptide sequence is the extracellular domain of the human FcRH3
CC protein of the invention.

XX
SQ Sequence 554 AA;

Query Match		36.8%;	Score 1150.5;	DB 7;	Length 554;
Best Local Similarity		45.5%;	Pred. No. 1.5e-75;		
Matches 250;		Conservative 73;	Mismatches 213;	Indels 13;	Gaps 7;
QY	21	PRPIFLQPPMTTVFQGRVTLTKGPRFYSPQ-KTKWYHRYLGEIIRTPDPNILEVQE	79		
DB	4	PKAVLLNPWPSTAPKGEKVALICSSISHSLAQGDYWH---DEKLKIKHDXI-QITE	59		
QY	80	SGEYEQAGQGPLSPVHLDSSASLILOAPLSVFEQDSVVLRCRAKAEVTLNNTIYKND	139		
DB	60	PNYQCKTRGSLSDAVHEFSPDWLIILQALHPFEGDNVILRCQKDNKTHQKXYKD	119		
QY	140	NVLAFLNKRTPHIFHACLKONGAYRCTYKESC---CPVSSNTVKIQVQEPFTRPVIRA	196		
DB	120	GKQLENSYLNLEKITVNSVSRONGKYHCTAYRKVFYILDIEVTSKPLNIQVQELFLHPVIRA	179		
QY	197	SSFQISGNPVTLCETQSLERSDVPVLPFRFRDDOTLGLGWSLSNFOITANWSKDSG	256		
DB	180	SSSTPIEGSPMTLTCETQSPQPDVQVQSLFRDSQTLGLGWSRSPRLQIPAMWTEDSG	239		
QY	257	FYWCXAATMPHSVSDSPRSMTQVO-IPASHPVLTLSPKALNTEGKVTVLHCETQEDSL	315		
DB	240	SWCCEVETVTHSIKKSLSRQIRVQVPVSVNVLNLEIRPTGGQLIEGENMVLICVAQSGG	299		
QY	316	RTLYRPFYHGVPLRHKSVRCERGASISFSLTT---ENSGNIYCTADNGLGAKPSKAVLS	372		
DB	300	TVTFSWHKEG-RVRSIGRKRTORSLLAELHLVLTVKESDAGRYVCAADNVHSPILSTWIRVT	358		
QY	373	VTVPVSHPVNLSSPEDLIFEKAKVTLHCEAQRGSLPILYQFHEDAALERRSANSAGGV	432		
DB	359	VRIPVSHPVLTTPRAHTVVGDLLELCELSRGSPPILYRPFYHEDVTILGNSAPSGGA	418		
QY	433	AISFSLTAHSGNYCTADNFGPQRKAVLSITVPVSHPVLTLSLSSAEALTFFEGATVTL	492		
DB	419	SPNLSLTAHSGNYSADNGLGAQHSHGVSLRVTPVPSRPVLTLPAPCAQAVVGDILLEL	478		
QY	493	HCEVORGSPQIILYQFYHEDMPVLSSTPSVGRVSFSLTECHSGNYCTADNFGPQRS	552		
DB	479	HCESLRGSPPILYWFYHEDTLGNISAHSGGASPNLSLTTEHSGNYSCEADNGLGAQHS	539		
QY	553	EVVSLFVTG	561		
DB	539	KVTLNVTG	547		

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Job time : 157 secs

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OM protein - protein search, using sw model

Run on: November 30, 2004, 11:39:56 ; Search time 39 Seconds

(without alignments)
1006.673 Million cell updates/sec

Title: US-09-724-254A-3

Perfect score: 3124

Sequence: 1 MLWVILLVLPVSGQFART.....AEPSLTHSPKFLFALSSFLP 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	12.4	261	US-09-245-764-7	Sequence 7, Appli
2	305.5	9.8	254	US-08-667-939A-3	Sequence 3, Appli
3	305.5	9.8	254	US-08-433-123-3	Sequence 3, Appli
4	304.5	9.7	254	US-08-667-939A-2	Sequence 2, Appli
5	304.5	9.7	254	US-08-433-123-2	Sequence 2, Appli
6	293	9.4	233	US-08-667-939A-6	Sequence 6, Appli
7	293	9.4	233	US-08-433-123-6	Sequence 6, Appli
8	292.5	9.4	254	US-08-667-939A-9	Sequence 9, Appli
9	292.5	9.4	254	US-08-433-123-9	Sequence 9, Appli
10	292	9.3	233	US-08-667-939A-5	Sequence 5, Appli
11	292	9.3	233	US-08-667-939A-8	Sequence 8, Appli
12	292	9.3	233	US-08-433-123-5	Sequence 5, Appli
13	292	9.3	233	US-08-433-123-8	Sequence 8, Appli
14	288.5	9.2	254	US-08-667-939A-4	Sequence 4, Appli
15	288.5	9.2	254	US-08-433-123-4	Sequence 4, Appli
16	286	9.2	233	US-08-667-939A-7	Sequence 7, Appli
17	286	9.2	233	US-08-433-123-7	Sequence 7, Appli
18	285.5	9.1	254	US-08-667-939A-1	Sequence 1, Appli
19	285.5	9.1	254	US-08-433-123-1	Sequence 1, Appli
20	275	8.8	197	US-08-788-954-2	Sequence 2, Appli
21	275	8.8	203	US-08-667-939A-20	Sequence 20, Appli
22	275	8.8	203	US-08-433-123-20	Sequence 20, Appli
23	274	8.8	174	US-09-245-764-8	Sequence 8, Appli
24	271	8.7	215	US-08-667-939A-18	Sequence 18, Appli
25	271	8.7	215	US-08-433-123-18	Sequence 18, Appli
26	269.5	8.6	199	US-08-768-964-12	Sequence 12, Appli
27	269.5	8.6	199	US-09-005-299-12	Sequence 12, Appli

28	269.5	8.6	199	3	US-09-515-431-12	Sequence 12, Appli
29	269.5	8.6	263	2	US-08-768-964-2	Sequence 2, Appli
30	269.5	8.6	263	3	US-09-005-299-2	Sequence 2, Appli
31	269.5	8.6	263	3	US-09-515-431-2	Sequence 2, Appli
32	267	8.5	197	2	US-08-756-387B-11	Sequence 11, Appli
33	267	8.5	197	3	US-09-285-873-11	Sequence 11, Appli
34	267	8.5	197	4	US-09-944-277A-11	Sequence 11, Appli
35	267	8.5	257	1	US-07-869-933-11	Sequence 11, Appli
36	267	8.5	257	2	US-08-756-387B-2	Sequence 2, Appli
37	267	8.5	257	3	US-09-103-663-11	Sequence 11, Appli
38	267	8.5	257	3	US-09-285-873-2	Sequence 2, Appli
39	267	8.5	257	4	US-08-897-956A-1	Sequence 1, Appli
40	267	8.5	257	4	US-09-944-277A-2	Sequence 2, Appli
41	267	8.5	978	4	US-08-897-956A-3	Sequence 3, Appli
42	266	8.5	307	2	US-08-332-562A-83	Sequence 83, Appli
43	265	8.5	193	2	US-08-765-536-1	Sequence 1, Appli
44	265	8.5	193	5	PCT-US95-08401-1	Sequence 1, Appli
45	257	8.2	261	2	US-08-332-562A-133	Sequence 133, App

ALIGNMENTS

RESULT 1
US-09-245-764-7
; Sequence 7, Application US/09245764
; Patent No. 6675105
; GENERAL INFORMATION:
; APPLICANT: Hogarth, P. Mark
; APPLICANT: Powell, Maree S.
; APPLICANT: McKenzie, Ian P.C.
; APPLICANT: Maxwell, Kelly F.
; APPLICANT: Garrett, Thomas P.J.
; APPLICANT: Epa, Vidana
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 4102-4
; CURRENT APPLICATION NUMBER: US/09/245,764
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/099,994
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: 60/073,972
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-764-7

Query Match 12.4%; Score 386; DB 4; Length 261;
Best Local Similarity 35.7%; Pred. No. 6.2e-27;
Matches 95; Conservative 40; Mismatches 121; Indels 10; Gaps 6;

Qy	20	TPRPIIFLOPPWTTFQGERVTLTCKGFRFSPQKTHRYLKGILRTPD---NILE 76
Db	1	TTKAVITLQPPVSVFQETVILHCEVLPGLSSSTQWFVN--GTATQSTPSYRITSAS 58
Qy	77	VQSGEYRCQAQSGPLSSPVHLDFFSASLILQAPLSVF-EGDSVULRCRAKAEVTLNVL 135
Db	59	VNDSGEYRCQGLSGRSDPTQLHHRGWLILQVSSRVFTEGEPLALRCHAWKDKLYNVL 118
Qy	136	YKNDNVLAFLNKETDHFHACIKDNGAYRCTGYKSCCPVSSNTVKIOVEPPTRPVL 195
Db	119	YRANGKFKPHWNSNLTILKTNISHNGTVHCSMGKH--RYTSAGISVTIVKELFPAPVL 176
Qy	196	ASSFQP-ISGNPVTLTCTQLSLERSDVLPRFFRDQTLGLGWSLSPNFQITAMWSKD 254
Db	177	ASVTSPLLEGNLVTLSCETKLLKQRPGLQLYFSGYMGSKTL-RGRNTSSSYQILTARRED 235
Qy	255	SGFWCKAATMPSVSDSPRSNIQV 280

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Db 236 SGLYWCBAATEDGNVLRSPLELQV 261

RESULT 2
US-08-667-939A-3
; Sequence 3, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-667-939A-3

Query Match 9.8%; Score 305.5; DB 2; Length 254;
Best Local Similarity 32.9%; Pred. No. 1.3e-19;
Matches 91; Conservative 37; Mismatches 102; Indels 47; Gaps 11;

QY 1 MLLWVILLVAPVSGQPARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVSAAGMTEDLPKAVVLEPQWRYVLEKDSVTLKCG--AYSPEDNSTQWF 61
QY 59 HRYLGKEILRETPDNILE-----VQESGEYRCQAQGSPLSSPVHLDFSSASLI 106
Db 62 HK-----ENLISSQASSYFIDAATVDSGSEYRCQTNLTSLSDPVQLEVQVGWLL 110
QY 107 LQAPLSVP-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKEIDFHIPACIKDNGAY 164
Db 111 LQAPRWVFKBEDPILHRCCHSWKNTALHKVTYLVQNGKDKRYFHNSDFHIPKATLKDSGSY 170
QY 165 RCTGYKESCCVSNVTVKIQVQEPFTRPVLRASSFQISGNPVTLTCTQLSERSDVPL 224
Db 171 FCRGLVGS-KNVSSETVNIITQGLA--VSTISFFP-PGYQVSF-CLVMVLLFAVDT-- 223
QY 225 RFRFRDDQTLGLGWSLSPNFQITAMMSKDSGFYCK 261
Db 224 -----GLYFSVKTNIIRSTRDWDKHKFKWK 249

RESULT 3
US-08-433-123-3
; Sequence 3, Application US/08433123
```

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; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-123-3

Query Match 9.8%; Score 305.5; DB 4; Length 254;
Best Local Similarity 32.9%; Pred. No. 1.3e-19;
Matches 91; Conservative 37; Mismatches 102; Indels 47; Gaps 11;

QY 1 MLLWVILLVAPVSGQPARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVSAAGMTEDLPKAVVLEPQWRYVLEKDSVTLKCG--AYSPEDNSTQWF 61
QY 59 HRYLGKEILRETPDNILE-----VQESGEYRCQAQGSPLSSPVHLDFSSASLI 106
Db 62 HK-----ENLISSQASSYFIDAATVDSGSEYRCQTNLTSLSDPVQLEVQVGWLL 110
QY 107 LQAPLSVP-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKEIDFHIPACIKDNGAY 164
Db 111 LQAPRWVFKBEDPILHRCCHSWKNTALHKVTYLVQNGKDKRYFHNSDFHIPKATLKDSGSY 170
QY 165 RCTGYKESCCVSNVTVKIQVQEPFTRPVLRASSFQISGNPVTLTCTQLSERSDVPL 224
Db 171 FCRGLVGS-KNVSSETVNIITQGLA--VSTISFFP-PGYQVSF-CLVMVLLFAVDT-- 223
QY 225 RFRFRDDQTLGLGWSLSPNFQITAMMSKDSGFYCK 261
Db 224 -----GLYFSVKTNIIRSTRDWDKHKFKWK 249

RESULT 4
US-08-667-939A-2
; Sequence 2, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
```

STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIORITY APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LWO=2A
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-2

Query Match 9.7%; Score 304.5; DB 2; Length 254;
Best Local Similarity 32.9%; Pred. No. 1.6e-19;
Matches 91; Conservative 38; Mismatches 101; Indels 47; Gaps 11;

QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPQ--KTKWY 58
DB 4 LLLPTALLLVAGNRTEDLPKAVVLEPQWYVLEKDSVTLKCOG--AYSPEDNSTQWF 61

QY 59 HRYLGKEILRETPDNILE-----VOESGEYRCQAGSPVHLDFFSSASLI 106
DB 62 HK-----ENLISSQASSYFIDAATVDDSGEYRCQNLSTLSDPVQLEVQVGWLL 110

QY 107 LQAPLSVFP-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRDTDFHIFHACLDKNGAY 164
DB 111 LQAPRWVFEEDPIHLRCHSWKNTALHKVTVLQNGKDRKYFHNSDFHIFKATLKDGSY 170

QY 165 RCTGYKESCCPVSSNTVKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVPL 224
DB 171 FCKGLVGS-KNVSSFTVNTIIQGLA--VSTNSGFPP-PGYQVSF-CLVMVLLFAVDT-- 223

QY 225 RFRFRDDOTLGLGWSLSPNFQITAMWSKDSGFYWK 261
DB 224 -----GLYFSVKTNRSTRDKWHDHFKWRK 249

RESULT 5
US-08-433-123-2
Sequence 2, Application US/08433123
Patent No. 644789
GENERAL INFORMATION:
APPLICANT: LWO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996

STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-667-939A-6

Query Match 9.4%; Score 293; DB 2; Length 233;
Best Local Similarity 34.7%; Pred. No. 1.6e-18;
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVLSAGMRTEDLPKAVVLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWP 61
QY 59 HRYLGKEILRETPDNILE-----VQESGEYRCQAQSPSSPVHLDFFSSASLI 106
Db 62 HN-----ENLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEHVHVGWLL 110
QY 107 LQAPLSVP-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKETDFHPIHACLKNGAY 164
Db 111 LQAPRWFKBEDPIHLRCHSWKNTALHKVTYLGKDKRKYFHNSDFHPIKATLKDSGSY 170
QY 165 RCTGYKSCCPVSSNTVKIQVQEPFTRPVLRASSFQISGNPVTLTCTQLSLERSDVPL 224
Db 171 FCRLGVSG-KNVSSETVNIITQGLA--VSTISSFSP-PGYQVSF-CLVNVLLFAVDVTGL 225
QY 225 RF 226
Db 226 YF 227

RESULT 7
US-08-433-123-6
; Sequence 6, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-667-939A-6

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-6

Query Match 9.4%; Score 293; DB 4; Length 233;
Best Local Similarity 34.7%; Pred. No. 1.6e-18;
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVLSAGMRTEDLPKAVVLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWP 61
QY 59 HRYLGKEILRETPDNILE-----VQESGEYRCQAQSPSSPVHLDFFSSASLI 106
Db 62 HN-----ENLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEHVHVGWLL 110
QY 107 LQAPLSVP-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKETDFHPIHACLKNGAY 164
Db 111 LQAPRWFKBEDPIHLRCHSWKNTALHKVTYLGKDKRKYFHNSDFHPIKATLKDSGSY 170
QY 165 RCTGYKSCCPVSSNTVKIQVQEPFTRPVLRASSFQISGNPVTLTCTQLSLERSDVPL 224
Db 171 FCRLGVSG-KNVSSETVNIITQGLA--VSTISSFSP-PGYQVSF-CLVNVLLFAVDVTGL 225
QY 225 RF 226
Db 226 YF 227

RESULT 8
US-08-667-939A-9
; Sequence 9, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-9

Query Match
Best Local Similarity 9.4%; Score 292.5; DB 2; Length 254;
Matches 89; Conservative 38; Mismatches 11; Indels 31; Gaps 11;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVLSAGMRTEDLPKAVVLEPQYRVLKDSVTLKCG--AYSPEDNSTQWF 61

QY 59 HRYLGEILRETPDNIL----EVQSGEYRCQAQSGPLSSPVHLDFFSSASLILOAPLSVF 114
Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118

QY 115 -EGSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTHPHACLKNGAYCTGYKES 172
Db 119 KEEDPIHLRCHSWKNTALHKVTYLONGKGRKYFHNSDFYIPKATLKDSGYFCRGLFGS 178

QY 173 CCPVSSNTVKIQVQEPFTRPVLRASSFPQISGNPVTLTCETQLSLERSDVLPRFRFRDD 232
Db 179 -KWSSEVNTITQGLA--VSTISSFPF-PGYQVSF-CLVMVLLFAVDT----- 223

QY 233 QTLGLGWSLSPNFQITAMWSKDSGFYCK 261
Db 224 ---GLYFSVKTNIRSTRDWDKHKFKWRK 249

RESULT 9
US-08-433-123-9
; Sequence 9, Application US/08433123
; Patent No. 644789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-123-9

Query Match
Best Local Similarity 9.4%; Score 292.5; DB 4; Length 254;
Matches 89; Conservative 38; Mismatches 11; Indels 31; Gaps 11;

Best Local Similarity 33.1%; Pred. No. 2e-18;
Matches 89; Conservative 38; Mismatches 11; Indels 31; Gaps 11;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVLSAGMRTEDLPKAVVLEPQYRVLKDSVTLKCG--AYSPEDNSTQWF 61

QY 59 HRYLGEILRETPDNIL----EVQSGEYRCQAQSGPLSSPVHLDFFSSASLILOAPLSVF 114
Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118

QY 115 -EGSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTHPHACLKNGAYCTGYKES 172
Db 119 KEEDPIHLRCHSWKNTALHKVTYLONGKGRKYFHNSDFYIPKATLKDSGYFCRGLFGS 178

QY 173 CCPVSSNTVKIQVQEPFTRPVLRASSFPQISGNPVTLTCETQLSLERSDVLPRFRFRDD 232
Db 179 -KWSSEVNTITQGLA--VSTISSFPF-PGYQVSF-CLVMVLLFAVDT----- 223

QY 233 QTLGLGWSLSPNFQITAMWSKDSGFYCK 261
Db 224 ---GLYFSVKTNIRSTRDWDKHKFKWRK 249

RESULT 10
US-08-667-939A-5
; Sequence 5, Application US/08667939A
; Patent No. 598166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-667-939A-5

Query Match
Best Local Similarity 35.5%; Pred. No. 1.9e-18;
Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVLSAGMRTEDLPKAVVLEPQYRVLKDSVTLKCG--AYSPEDNSTQWF 61

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QY 59 HRYLGKEILRETPDNIL-----EVOESGEYRCOAGSPSSPVHLDPSASLILOAPLSVF 114
DB 62 H---NESLISSQASSYFIDATVNDSGEYRCQTNLSTLSDPVQLEVHIGWLLQAPRWVF 118
QY 115 -EGSVVLRCAKAEVTLNNTIY-KNDNVLAFLNKRTRDFHHPHACLKNDGAYRCTGYKES 172
DB 119 KEEDPIHLRCHSWKNTALHKVTYLQNGKDRKYFHNSDFHHPKATLKDSGYSFCRGLVGS 178
QY 173 CCPVSSNTVKIQOEPETRPVLRASSFPQISGNPVTLTCTQSLERSDVLPLRF 226
DB 179 -KNVSSETVNTITQGLA--VSTISSFSF-PGYQVSF-CLVMVLLFAVDITGLYF 227

RESULT 11
US-08-667-939A-8
; Sequence 8, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-667-939A-8

Query Match 9.3%; Score 292; DB 2; Length 233;
Best Local Similarity 35.5%; Pred. No. 1.9e-18;
Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;

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DB 4 LLLPTALLLVSAQWRTEFLKAVFLEPQWYSVLEKDSVTLKQCG--AYSPEDNSTQWF 61
QY 59 HRYLGKEILRETPDNIL-----EVOESGEYRCOAGSPSSPVHLDPSASLILOAPLSVF 114
DB 62 H---NESLISSQASSYFIDATVNDSGEYRCQTNLSTLSDPVQLEVHIGWLLQAPRWVF 118
QY 115 -EGSVVLRCAKAEVTLNNTIY-KNDNVLAFLNKRTRDFHHPHACLKNDGAYRCTGYKES 172
DB 119 KEEDPIHLRCHSWKNTALHKVTYLQNGKDRKYFHNSDFHHPKATLKDSGYSFCRGLVGS 178
QY 173 CCPVSSNTVKIQOEPETRPVLRASSFPQISGNPVTLTCTQSLERSDVLPLRF 226
DB 179 -KNVSSETVNTITQGLA--VSTISSFSF-PGYQVSF-CLVMVLLFAVDITGLYF 227

RESULT 13
US-08-433-123-8
; Sequence 8, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS

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DB 179 -KNVSSETVNTITQGLA--VSTISSFSF-PGYQVSF-CLVMVLLFAVDITGLYF 227

RESULT 12
US-08-433-123-5
; Sequence 5, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-123-5

Query Match 9.3%; Score 292; DB 4; Length 233;
Best Local Similarity 35.5%; Pred. No. 1.9e-18;
Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;

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DB 4 LLLPTALLLVSAQWRTEFLKAVFLEPQWYSVLEKDSVTLKQCG--AYSPEDNSTQWF 61
QY 59 HRYLGKEILRETPDNIL-----EVOESGEYRCOAGSPSSPVHLDPSASLILOAPLSVF 114
DB 62 H---NESLISSQASSYFIDATVNDSGEYRCQTNLSTLSDPVQLEVHIGWLLQAPRWVF 118
QY 115 -EGSVVLRCAKAEVTLNNTIY-KNDNVLAFLNKRTRDFHHPHACLKNDGAYRCTGYKES 172
DB 119 KEEDPIHLRCHSWKNTALHKVTYLQNGKDRKYFHNSDFHHPKATLKDSGYSFCRGLVGS 178
QY 173 CCPVSSNTVKIQOEPETRPVLRASSFPQISGNPVTLTCTQSLERSDVLPLRF 226
DB 179 -KNVSSETVNTITQGLA--VSTISSFSF-PGYQVSF-CLVMVLLFAVDITGLYF 227

RESULT 13
US-08-433-123-8
; Sequence 8, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS

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NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-8

Query Match          9.3%; Score 292; DB 4; Length 233;
Best Local Similarity 35.5%; Pred.No.1.9e-16;
Matches      83; Conservative    34; Mismatches   99; Indels    18; Gaps    10;

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RESULT 14
US-08-667-939A-4
Sequence 4, Application US/08667939A
Patent No. 5998166
GENERAL INFORMATION:
APPLICANT: LUO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-4

Query Match          9.2%; Score 288.5; DB 4; Length 254;
Best Local Similarity 33.1%; Pred.No. 4.6e-18;
Matches 89; Conservative 37; Mismatches 112; Indels 31; Gaps 11;

QY 1 MLLWVLLVLPVSGQPARTPRPIELFQPPHTTYFQGERVTLCKGPRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVSGMRTEDLPRAVVELEPQYRVLEKDSVTLKCG--AYSPEDNSTQWF 61
QY 59 HRYLGKEILRETPDNIL-----EVQESGEYRCQACQSPLSFVHLDFFSSASLIILQAPLSVF 114
Db 62 H--NESLISSQASSYPTDAATVDSDGEYRCQTNLSTLSDPVQLEVHIGWLLQAPRWVF 118
QY 115 -EGDSVILRCRAKAEVTLNNTIY-KNDNVLAFLNKRTPDFHPIHACLKDNCAVRCCTGYKES 172
Db 119 KEEDPIHLRCHSWKNTALHKVTLQNGKGRKYSHHNSDFYIPKATLKDSGYFCRGLFGS 178
QY 173 CCPVSSNTVKIQOEPPTTRPVLRASSFQPISGNPNVTLTCTQLSLERSDVLPRFRFRDD 232
Db 179 -KNYSSEVNTITQGLA--VSTISSFPF-PGYQVSP-CLVMVLLFAVDT----- 223
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Search completed: November 30, 2004, 11:51:54
Job time : 40 secs
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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 30, 2004, 11:44:31 ; Search time 144 Seconds

(without alignments)
1458.190 Million cell updates/sec

Title: US-09-724-254A-3

Perfect score: 3124

Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1575965 seqs, 354694765 residues

Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3111	99.6	592	15	US-10-057-475B-10461
3	3111	99.6	592	15	US-10-154-884B-10461
4	3111	99.6	592	15	US-10-403-847-8
5	3111	99.6	592	16	US-10-764-324-10461
6	2950	94.4	759	14	US-10-040-862-10460
7	2950	94.4	759	15	US-10-057-475B-10460
8	2950	94.4	759	15	US-10-154-884B-10460
9	2950	94.4	759	15	US-10-403-847-7
10	2950	94.4	759	16	US-10-764-324-10460
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12	2950	94.4	977	14	US-10-241-220-97
13	2950	94.4	977	15	US-10-057-475B-10462

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Sequence 10462, A
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Sequence 4, Appli
Sequence 6, Appli
Sequence 94, Appl
Sequence 2, Appli
Sequence 4774, Ap
Sequence 10463, A
Sequence 10463, A
Sequence 10463, A
Sequence 286, App
Sequence 431, App
Sequence 2410, Ap
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Sequence 96, Appl
Sequence 98, Appl
Sequence 10, Appl
Sequence 100, App
Sequence 11043, A
Sequence 10464, A
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Sequence 11039, A
Sequence 10464, A
Sequence 458, App
Sequence 11052, A

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US-10-154-884B-10464
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US-10-764-324-10464
US-10-363-829-458
US-10-154-884B-11052

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17 2950 94.4 977 17
18 2924.5 93.6 790 15
19 1854 59.3 438 15
20 1502 48.1 317 15
21 1193.5 38.2 582 15
22 1193.5 38.2 707 15
23 1193.5 38.2 734 14
24 1193.5 38.2 734 15
25 1193.5 38.2 734 15
26 1193.5 38.2 734 16
27 900 28.8 181 16
28 900 28.8 181 16
29 847.5 27.1 639 16
30 826.5 26.5 515 14
31 826.5 26.5 515 15
32 826.5 26.5 515 15
33 826.5 26.5 515 16
34 803.5 25.7 421 15
35 803.5 25.7 421 15
36 791 25.3 152 15
37 786.5 25.2 421 15
38 783.5 25.1 445 15
39 773.5 24.8 508 14
40 773.5 24.8 508 15
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44 729.5 23.4 327 15
45 713 22.8 397 15

ALIGNMENTS

RESULT 1

US-10-040-862-10461
; Sequence 10461, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-01352005
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416

QY 541 CTADNGFGPQSEVWSLFTVTKCWLASKPPLAEFSLTHSFKNLPALSSFLP 592
DB 541 CTADNGFGPQSEVWSLFTVTKCWLASHPLAEFSLTHSFKNLPALSSFLP 592

RESULT 3
US-10-154-884B-10461
; Sequence 10461, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10461
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10461

Query Match 99.6%; Score 3111; DB 15; Length 592;
Best Local Similarity 99.7%; Pred. No. 1.7e-232;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPIHACLKDNAGYRCTGYKSCCPVSSNT 180
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QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSIITPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSIITPVSHPVLTLSA 480
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DB 541 CTADNGFGPQSEVWSLFTVTKCWLASHPLAEFSLTHSFKNLPALSSFLP 592

RESULT 4
US-10-403-847-8
; Sequence 8, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICE VARIANTS OF A HUMAN
; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOLOGOBULIN FOLDS, BGS5G AND BGS5S
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-8

Query Match 99.6%; Score 3111; DB 15; Length 592;
Best Local Similarity 99.7%; Pred. No. 1.7e-232;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFGERVTLTKGFRFYSPQTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFGERVTLTKGFRFYSPQTKWYHR 60
QY 61 YLCKEILRETPDNILVEQSEGYRCQAGSPSSPVHLDFFSASLILQAPLSVFEQDSV 120
DB 61 YLCKEILRETPDNILVEQSEGYRCQAGSPSSPVHLDFFSASLILQAPLSVFEQDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPIHACLKDNAGYRCTGYKSCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPIHACLKDNAGYRCTGYKSCCPVSSNT 180
QY 181 VKIQVEPPTRPVLRASSFQPSGNPVTLCETQLSLERSDVPFRFRDDQTLGLWS 240
DB 181 VKIQVEPPTRPVLRASSFQPSGNPVTLCETQLSLERSDVPFRFRDDQTLGLWS 240
QY 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVISDSFRSWIQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVISDSFRSWIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTRKVTLCHECTQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTSTNSGNYYCTADNG 360
DB 301 GTRKVTLCHECTQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTSTNSGNYYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEKAKVTLHCEAQRGSLPILYQPHHEDAA 420

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Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLI FEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Qy 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHPVLTLSA 480
Db 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHPVLTLSA 480
Qy 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVFSFSLTEGHSNGY 540
Db 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVFSFSLTEGHSNGY 540
Qy 541 CTADNGFGPORSSEVSVLFTVKCKWVLASKPPLAEFSLTHSFKNLFASSFLP 592
Db 541 CTADNGFGPORSSEVSVLFTVKCKWVLASHPPLAEFSLTHSFKNLFASSFLP 592

RESULT 5
US-10-764-324-10461
; Sequence 10461, Application US/10764324
; Publication No. US2004017539A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10461
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10461

Query Match 99.6%; Score 3111; DB 16; Length 592;
Best Local Similarity 99.7%; Pred. No. 1,7e-232;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MLLWVILLVAPVSGQPARTPRIIFLOPPWTTVFGERVTLTKCKGRFYSPOKTKWYH 60
Db 1 MLLWVILLVAPVSGQPARTPRIIFLOPPWTTVFGERVTLTKCKGRFYSPOKTKWYH 60
Qy 61 YLCKEILRETPDNILOEVSGEYRCQAQGSPLSSPVHLDFSSASLILOAPLSVFEGDSV 120
Db 61 YLCKEILRETPDNILOEVSGEYRCQAQGSPLSSPVHLDFSSASLILOAPLSVFEGDSV 120
Qy 121 LRCRAEAVTLNNTIYKNDNVLAFLNKRDTDFH;PHACLKNDGAYRCTGYKESCCPVSSNT 180
```

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Db 121 LRCRAEAVTLNNTIYKNDNVLAFLNKRDTDFH;PHACLKNDGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQOEFTPEPVLRASSQFQISGNPVTLTCETOLSLERSDVLPRFRFRDDQTLGLGWS 240
Db 181 VKIQOEFTPEPVLRASSQFQISGNPVTLTCETOLSLERSDVLPRFRFRDDQTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPSHVSISDSPRSIVQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPSHVSISDSPRSIVQVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETOEDSLRTLRYFHYHGVPLRHKSVCRCGASISFSLTTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETOEDSLRTLRYFHYHGVPLRHKSVCRCGASISFSLTTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLI FEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLI FEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Qy 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHPVLTLSA 480
Db 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHPVLTLSA 480
Qy 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVFSFSLTEGHSNGY 540
Db 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVFSFSLTEGHSNGY 540
Qy 541 CTADNGFGPORSSEVSVLFTVKCKWVLASKPPLAEFSLTHSFKNLFASSFLP 592
Db 541 CTADNGFGPORSSEVSVLFTVKCKWVLASHPPLAEFSLTHSFKNLFASSFLP 592

RESULT 6
US-10-040-862-10460
; Sequence 10460, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
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; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-10460

Query Match
Best Local Similarity 94.4%; Score 2950; DB 14; Length 759;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLWLWILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKMYHR 60
DB 1 MLWLWILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKMYHR 60
QY 61 YLCKEILRETPDNILVQESGVRCAQGSPLSSPVHLDFSSASLILQAPLSVEGDSV 120
DB 61 YLCKEILRETPDNILVQESGVRCAQGSPLSSPVHLDFSSASLILQAPLSVEGDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRDTDFH PHACLKNDGAYRCTGYKSCCPVSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRDTDFH PHACLKNDGAYRCTGYKSCCPVSNT 180
QY 181 VKIQVEPTPRVLRASSQFPIISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLWS 240
DB 181 VKIQVEPTPRVLRASSQFPIISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLWS 240
QY 241 LSPNFOITAMWSKDSGFYWKCAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYWKCAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLRYFVHEGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYFVHEGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSPLILYQFHHEDAA 420
DB 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSPLILYQFHHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 480
QY 481 EALTPEGATVTLHCEVQRGSQILYQFYHEDMPLVSSSTPSVGRVSFSLTEHSGNYY 540
DB 481 EALTPEGATVTLHCEVQRGSQILYQFYHEDMPLVSSSTPSVGRVSFSLTEHSGNYY 540
QY 541 CTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 572
DB 541 CTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 568
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RESULT 7

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US-10-057-475B-10460
; Sequence 10460, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
```

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; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-10460
```

Query Match 94.4%; Score 2950; DB 15; Length 759;

Best Local Similarity 98.4%; Pred. No. 7.1e-220;

Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLWLWILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKMYHR 60

DB 1 MLWLWILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKMYHR 60

QY 61 YLCKEILRETPDNILVQESGVRCAQGSPLSSPVHLDFSSASLILQAPLSVEGDSV 120

DB 61 YLCKEILRETPDNILVQESGVRCAQGSPLSSPVHLDFSSASLILQAPLSVEGDSV 120

QY 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRDTDFH PHACLKNDGAYRCTGYKSCCPVSNT 180

DB 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRDTDFH PHACLKNDGAYRCTGYKSCCPVSNT 180

QY 181 VKIQVEPTPRVLRASSQFPIISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLWS 240

DB 181 VKIQVEPTPRVLRASSQFPIISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLWS 240

QY 241 LSPNFOITAMWSKDSGFYWKCAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE 300

DB 241 LSPNFOITAMWSKDSGFYWKCAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE 300

QY 301 GTKVTLHCETQEDSLRTLRYFVHEGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360

DB 301 GTKVTLHCETQEDSLRTLRYFVHEGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360

QY 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSPLILYQFHHEDAA 420

DB 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSPLILYQFHHEDAA 420

QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 480

DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 480

QY 481 EALTPEGATVTLHCEVQRGSQILYQFYHEDMPLVSSSTPSVGRVSFSLTEHSGNYY 540

DB 481 EALTPEGATVTLHCEVQRGSQILYQFYHEDMPLVSSSTPSVGRVSFSLTEHSGNYY 540

QY 541 CTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 572

DB 541 CTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 568

RESULT 8

US-10-154-884B-10460
; Sequence 10460, Application US/10154884B
; Publication No. US2004000561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR FILING DATE: 2002-05-23
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10460

Query Match 94.4%; Score 2950; DB 15; Length 759;
Best Local Similarity 98.4%; Pred. No. 7.1e-220;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPMTTVFQGERVTLCKGFRFYSPQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPMTTVFQGERVTLCKGFRFYSPQKTKWYHR 60
QY 61 YLGEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVV 120
DB 61 YLGEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPFRFRDDQTLGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPFRFRDDQTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVLSDSRSMIOVQIPASHVPLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVLSDSRSMIOVQIPASHVPLTLSPEKALNFE 300
QY 301 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVCRCGASISFSLTTENSGNYCTADNG 360
DB 301 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVCRCGASISFSLTTENSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTVPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

RESULT 9

US-10-403-847-7
; Sequence 7, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICING VARIANTS OF A HUMAN
; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOLOGICAL FOLDS, BGS5G AND BGS5I
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patent version 3.2
; SEQ ID NO 7
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-7

Query Match 94.4%; Score 2950; DB 15; Length 759;
Best Local Similarity 98.4%; Pred. No. 7.1e-220;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPMTTVFQGERVTLCKGFRFYSPQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPMTTVFQGERVTLCKGFRFYSPQKTKWYHR 60
QY 61 YLGEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVV 120
DB 61 YLGEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPFRFRDDQTLGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPFRFRDDQTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVLSDSRSMIOVQIPASHVPLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVLSDSRSMIOVQIPASHVPLTLSPEKALNFE 300
QY 301 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVCRCGASISFSLTTENSGNYCTADNG 360
DB 301 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVCRCGASISFSLTTENSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTVPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGPGPORSKAVSLSVTVPVSHVPLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGPGPORSKAVSLSVTVPVSHVPLTLSA 480

Db 421 LERRSANGGVAISFSLTAHSGNYCTADNGFGPQRKAVSLSVTVVSHVLTSSA 480
QY 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
Db 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
QY 541 CTADNGFGPQRSEVSLFVTGKCVLASKPPL 572
Db 541 CTADNGFGPQRSEVSLFVTGKCVLASKPPL 572

RESULT 10

US-10-764-324-10460
; Sequence 10460, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: 2004-01-23
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10457
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10460

Query Match 94.4%; Score 2950; DB 16; Length 759;
Best Local Similarity 98.4%; Pred. No. 7,1e-220;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLWLTVLLVAPVSGFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPOKTKWYHR 60
Db 1 MLWLTVLLVAPVSGFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPOKTKWYHR 60
QY 61 YLKGKILRTPDNILEVQSGEYRCQAQGSPLSSPVHLDFSSASILQAPLSVFFGDSV 120
Db 61 YLKGKILRTPDNILEVQSGEYRCQAQGSPLSSPVHLDFSSASILQAPLSVFFGDSV 120
QY 121 LCRARAEVTLNNTIYKNDNVLAFLNKRDFHPIACLDKNGAYRCTGYKESCCFVSNT 180
Db 121 LCRARAEVTLNNTIYKNDNVLAFLNKRDFHPIACLDKNGAYRCTGYKESCCFVSNT 180
QY 181 VKIQVQEPTRPVLRASSFPQISGNPVTLTCTQTSLERSDVLPRFRFRDDQTLGLWS 240

Db 181 VKIQVQEPTRPVLRASSFPQISGNPVTLTCTQTSLERSDVLPRFRFRDDQTLGLWS 240
QY 241 LSPNQITAMWSKDSGFYWCKAATMPHSVISDSRSMIQVOIPASHPVLTLSPEKALNFE 300
Db 241 LSPNQITAMWSKDSGFYWCKAATMPHSVISDSRSMIQVOIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYYCTADNG 360
Db 301 GTKVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYYCTADNG 360
QY 361 LGAKPSKAVSLSVTVVSHVLTSSPEDLLPEGAKVTLHCEAQRGSLPILYQFHHEDAA 420
Db 361 LGAKPSKAVSLSVTVVSHVLTSSPEDLLPEGAKVTLHCEAQRGSLPILYQFHHEDAA 420
QY 421 LERRSANGGVAISFSLTAHSGNYCTADNGFGPQRKAVSLSVTVVSHVLTSSA 480
Db 421 LERRSANGGVAISFSLTAHSGNYCTADNGFGPQRKAVSLSVTVVSHVLTSSA 480
QY 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
Db 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
QY 541 CTADNGFGPQRSEVSLFVTGKCVLASKPPL 572
Db 541 CTADNGFGPQRSEVSLFVTGKCVLASKPPL 572

RESULT 11

US-10-040-862-10462
; Sequence 10462, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT

ORGANISM: Homo sapiens
 US-10-040-862-10462
 Query Match 94.4%; Score 2950; DB 14; Length 977;
 Best Local Similarity 98.4%; Pred. No. 1e-219;
 Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
 QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGRFPYSPQTKWYHR 60
 DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGRFPYSPQTKWYHR 60
 QY 61 YLGEILRETPDNLILEVOESGEYRCQAGSPVHLDFSSASLILQAPLSVFEQDSVV 120
 DB 61 YLGEILRETPDNLILEVOESGEYRCQAGSPVHLDFSSASLILQAPLSVFEQDSVV 120
 QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPHIFACLKONGAYRCTGYKESCCPVSSNT 180
 DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPHIFACLKONGAYRCTGYKESCCPVSSNT 180
 QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETOLSERSDVPLRFRFRDDQTLGLWS 240
 DB 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETOLSERSDVPLRFRFRDDQTLGLWS 240
 QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOVOIPASHPVLTLSPEKALNFE 300
 DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOVOIPASHPVLTLSPEKALNFE 300
 QY 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
 DB 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
 QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
 DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
 QY 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
 DB 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
 QY 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPVSSSTPSVGRVSFSLTEGHSNYY 540
 DB 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPVSSSTPSVGRVSFSLTEGHSNYY 540
 QY 541 CTADNGFGPQRSSEVVSFLVTGKWCWLASKPPL 572
 DB 541 CTADNGFGPQRSSEVVSFLVTGKWCWLASKPPL 568
 RESULT 12
 US-10-241-220-97
 ; Sequence 97, Application US/10241220
 ; Publication No. US20030148408A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Frantz, Gretchen
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Phillips, Heidi
 ; APPLICANT: Polakis, Paul
 ; APPLICANT: Spencer, Susan
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wu, Thomas
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
 ; TREATMENT OF TUMOR
 ; FILE REFERENCE: P501081-US
 ; CURRENT APPLICATION NUMBER: US/10/241,220
 ; CURRENT FILING DATE: 2002-12-13
 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO 97
 ; LENGTH: 977
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-241-220-97

Query Match 94.4%; Score 2950; DB 14; Length 977;
 Best Local Similarity 98.4%; Pred. No. 1e-219;
 Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
 QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGRFPYSPQTKWYHR 60
 DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGRFPYSPQTKWYHR 60
 QY 61 YLGEILRETPDNLILEVOESGEYRCQAGSPVHLDFSSASLILQAPLSVFEQDSVV 120
 DB 61 YLGEILRETPDNLILEVOESGEYRCQAGSPVHLDFSSASLILQAPLSVFEQDSVV 120
 QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPHIFACLKONGAYRCTGYKESCCPVSSNT 180
 DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPHIFACLKONGAYRCTGYKESCCPVSSNT 180
 QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETOLSERSDVPLRFRFRDDQTLGLWS 240
 DB 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETOLSERSDVPLRFRFRDDQTLGLWS 240
 QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOVOIPASHPVLTLSPEKALNFE 300
 DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOVOIPASHPVLTLSPEKALNFE 300
 QY 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
 DB 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
 QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
 DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
 QY 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
 DB 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
 QY 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPVSSSTPSVGRVSFSLTEGHSNYY 540
 DB 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPVSSSTPSVGRVSFSLTEGHSNYY 540
 QY 541 CTADNGFGPQRSSEVVSFLVTGKWCWLASKPPL 572
 DB 541 CTADNGFGPQRSSEVVSFLVTGKWCWLASKPPL 568
 RESULT 13
 US-10-057-475B-10462
 ; Sequence 10462, Application US/10057475B
 ; Publication No. US2004002068A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Clapper, Jonathan David
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Ordonez, Nadia
 ; APPLICANT: Carter, Lauren
 ; APPLICANT: McNeill, Patricia Dianne
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
 ; TITLE OF INVENTION: Hematological Malignancies
 ; FILE REFERENCE: 014058-014402US
 ; CURRENT APPLICATION NUMBER: US/10/057,475B
 ; CURRENT FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: US 60/186,126
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: US 60/190,479
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: US 60/200,545
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: US 60/200,303
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-10462

Query Match 94.4%; Score 2950; DB 15; Length 977;
Best Local Similarity 98.4%; Pred. No. 1e-219;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPOKTKWYHR 60

QY 61 YLKGKILRETPDNLIVQESGEYRCQAQSPVHLDFSSASLILQAPLSVEGDSVV 120
DB 61 YLKGKILRETPDNLIVQESGEYRCQAQSPVHLDFSSASLILQAPLSVEGDSVV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACIKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACIKONGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVOEPFTRPVLASSQFISGNPVTTCETQLSLERSDVLRRFRFRDDOTLGLWS 240
DB 181 VKIQVOEPFTRPVLASSQFISGNPVTTCETQLSLERSDVLRRFRFRDDOTLGLWS 240

QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVIDSPPRSWIOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVIDSPPRSWIOVQIPASHPVLTLSPEKALNFE 300

QY 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCGASISPSLTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCGASISPSLTENSNGNYCTADNG 360

QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 480

QY 481 EALTTEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALTTEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540

QY 541 CTADNGFGQPSGVSVSLFVTGKCVLASKPPL 572
DB 541 CTADNGFGQPSGVSVSLFVT---VPVSRPIL 568

RESULT 14
US-10-154-884B-10462
; Sequence 10462, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10462

Query Match 94.4%; Score 2950; DB 15; Length 977;
Best Local Similarity 98.4%; Pred. No. 1e-219;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPOKTKWYHR 60

QY 61 YLKGKILRETPDNLIVQESGEYRCQAQSPVHLDFSSASLILQAPLSVEGDSVV 120
DB 61 YLKGKILRETPDNLIVQESGEYRCQAQSPVHLDFSSASLILQAPLSVEGDSVV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACIKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACIKONGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVOEPFTRPVLASSQFISGNPVTTCETQLSLERSDVLRRFRFRDDOTLGLWS 240
DB 181 VKIQVOEPFTRPVLASSQFISGNPVTTCETQLSLERSDVLRRFRFRDDOTLGLWS 240

QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVIDSPPRSWIOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVIDSPPRSWIOVQIPASHPVLTLSPEKALNFE 300

QY 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCGASISPSLTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCGASISPSLTENSNGNYCTADNG 360

QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 480

QY 481 EALTTEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540

Db 541 CTADNGFGPQSEVVSLFVT-----VPVSRPIL 568

Search completed: November 30, 2004, 11:54:25
Job time : 146 secs

Db 481 EALTFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTECHSGNYY 540

Qy 541 CTADNGFGPQSEVVSLFVTCKWVLASKPPL 572

Db 541 CTADNGFGPQSEVVSLFVT-----VPVSRPIL 568

RESULT 15

US-10-403-847-9

; Sequence 9, Application US/10403847

; Publication No. US20040030098A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICER VARIANTS OF A HUMAN

; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS, BGSSG AND BGSSH

; FILE REFERENCE: D0228 NP

; CURRENT APPLICATION NUMBER: US/10/403,847

; CURRENT FILING DATE: 2003-03-28

; PRIOR APPLICATION NUMBER: U.S. 60/369,671

; PRIOR FILING DATE: 2002-03-29

; PRIOR APPLICATION NUMBER: U.S. 60/371,420

; PRIOR FILING DATE: 2002-04-10

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 9

; LENGTH: 977

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-403-847-9

Query Match 94.4%; Score 2950; DB 15; Length 977;

Best Local Similarity 98.4%; Pred. No. le-219;

Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPQTKWYHR 60

Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPQTKWYHR 60

Qy 61 YLGEILLRETPDNIIEVOESGEYECQAGSPVHLDFSSASLILQAPLSVFGDSVY 120

Db 61 YLGEILLRETPDNIIEVOESGEYECQAGSPVHLDFSSASLILQAPLSVFGDSVY 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180

Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180

Qy 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETOLSLERSDVLPRFRFRDDDTLGLGWS 240

Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETOLSLERSDVLPRFRFRDDDTLGLGWS 240

Qy 241 LSPNFOITAMWSKDSGFYWKAAATMPHVSIDSRSWIOQIIPASHPVLTLSPEKALNFE 300

Db 241 LSPNFOITAMWSKDSGFYWKAAATMPHVSIDSRSWIOQIIPASHPVLTLSPEKALNFE 300

Qy 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360

Db 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360

Qy 361 LGARPSKAVSLSVTVVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAA 420

Db 361 LGARPSKAVSLSVTVVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAA 420

Qy 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSIITVPVSHVLTLSA 480

Db 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSIITVPVSHVLTLSA 480

Qy 481 EALTFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTECHSGNYY 540

Db 481 EALTFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTECHSGNYY 540

Qy 541 CTADNGFGPQSEVVSLFVTCKWVLASKPPL 572

Db 541 CTADNGFGPQSEVVSLFVTCKWVLASKPPL 572